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## ALIGNMENTS

RESULT 1 AAB28406 Jefferson RA, 17-MAR-1999; AAB28406 standard; Thermotoga maritima. AAB28406; 16-MAR-2000; 2000WO-US007107 21-SEP-2000. WO200055333-A1. transgenic insect; marker; glucuronide detoxification Pseudomonas; Microbial; beta-glucoronidase; Thermotoga maritima beta-glucoronidase. 26-JAN-2001 (CAMB-) CAMBIA BIOSYSTEMS LLC. (first Staphylococcus; Mayer JE; 99US-00270957. protein; entry) 563 e; GUS; Enterobacter; Salmonella; Thermotoga; transgenic plant; bi A bioindicator;

Novel microbial beta-glucuronidase genes and gene products used as reporter/effector molecule, as diagnostic tool, in positive selection, to target molecules to specific cells and to detect and track linked genes.

WPI; 2000-647075/62. N-PSDB; AAA07937.

Claim 3; Fig 5B; 116pp; English.

The present sequence is a microbial beta-glucuronidase (GUS) protein. GUS genes were obtained from six different genera: Enterobacter/Salmonella, Pseudomonas, Salmonella, Staphylococcus and Thermotoga. Microbial GUS car be used as a reporter/effector molecule for transgenic constructions and in in vitro diagnostic applications. It may also be used to generate sentinel plants that serve as bioindicators of environmental status. It may be used to generate transgenic insects for tracking insect populations or to facilitate the development of a bioassay for compounds that affect molecules critical for insect development (e.g. juvenile hormone). Secreted GUS may also serve as a marker for beneficial fungi destined for release into the environment. In animal systems, can GUS

Bacterial

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RESULT 2
ADN20342
ID ADN2
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Best Local S
Matches 563
Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (e.g. toxin glucuronide) and to examine conjugation patterns of glucuronides. Microbial GUS may also be used in traditional medical diagnostic assays, for drug testing, pharmacokinetic studies, bioavailability studies, diagnosis of diseases and syndromes, following progression of disease or its response to therapy. Microbial GUS has increased thermal stability, high turnover number and enzymatic activity. It is highly specific for the substrate and water soluble, and the
                                                                                                                  Bacterial
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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 2995; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to CC provide for expression of a polynuclectide encoding a polypeptide from a CC microbial source. The invention also relates to a transformed plant CC comprising the recombinant DNA construct and a method of producing a transformed plant to the method of producing a transformed plant CC such as maize or soybean. The method of producing a transformed plant CC having an improved property comprises transformed plant with the recombinant DNA construct and growing the transformed plant with the construct and growing the transformed plant with the recombinant DNA construct is useful for improving plants with the improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, conditions are combination, modified seed cold, heat or drought tolerance, to providing recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress completed in the invention. Note: The sequence data for this patent did not compart of the printed specification but was obtained in electronic commat from USPTO at sequence.

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RESULT 3
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ID AAW9
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 Query Match
Best Local Similarity
                                                                                                                                 This invention describes a novel secreted form of Bacillus sp. beta glucuronidase (BoGUS). The microbial BoGUS polypeptide can be used reporter/effector molecule and as a diagnostic tool. The products o invention can be used as markers for transgene constructions, e.g. plants or insects. They can also be used for the cleavage and detoxification of glucuronides and to examine conjugation patterns
                                                                       Sequence
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Similarity 35.6%; Pr
21; Conservative 93;
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Pred. No. 5.1e-67;
3; Mismatches 224;
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glucuronidase (BoGUS). The microbial BoGUS polypeptide can be used as
reporter/effector molecule and as a diagnostic tool. The products of
invention can be used as markers for transgene constructions, e.g. in
plants or insects. They can also be used for the cleavage and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GUS; BoGUS; beta-glucuronidase; secreted; reporter molecule; marker; receptor molecule; diagnostic tool; transgene construction; plant; insect; cleavage; detoxification; glucuronide.
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HKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDV
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                                                                                              KFLINNKPFYFKGFGKHEDTPINGRGFNEASNVMDFNILKWIGANSFRTAHYPYSEELMR
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Matches 221; Conser
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 602
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                                                                                                       Novel microbial beta-glucuronidase genes and gene products used as reporter/effector molecule, as diagnostic tool, in positive selection, target molecules to specific cells and to detect and track linked gene
                                                           Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microbial; beta-glucoronidase; GUS; Enterobacter; Salmonella; Pseudomonas; Staphylococcus; Thermotoga; transgenic plant; bitransgenic insect; marker; glucuronide detoxification.
                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                Jefferson RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes were obtained from six different genera: Enterobacter/Salmonella, CC Pseudomonas, Salmonella, Staphylococcus and Thermotoga. Microbial GUS can be used as a reporter/effector molecule for transgenic constructions and in vitro diagnostic applications. It may also be used to generate CC sentinel plants that serve as bioindicators of environmental status. It may be used to generate transgenic insects for tracking insect CC populations or to facilitate the development of a bioassay for compounds that affect molecules critical for insect development (e.g. juvenile cc hormone). Secreted GUS may also serve as a marker for beneficial fungi destined for release into the environment. In animal systems, secreted GUS may be used to achieve extracellular detoxification of glucuronides (e.g. toxin glucuronide) and to examine conjugation patterns of glucuronides. Microbial GUS may also be used in traditional medical diagnostic assays, for drug testing, pharmacokinetic studies, bioavailability studies, diagnosis of diseases and syndromes, following progression of disease or its response to therapy. Microbial GUS has increased thermal stability, high turnover number and enzymatic activity. Substrate and water soluble, and the
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                                                                           GFHDIDPVMFTEEYQVEYYQANHVVFDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVF
                                                                                                                GIHYDPPOMFSEEYOAELVEKTIRLLLKKDYIIGTHVWAFADFKTPONVRRPILNHKGVF
                                                                                                                                                       VAELIDVIALNRYNGWYFDGGDLEAAKVHLR--
                                                                                                                                                                                       ALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHR----KPIFVTEFGADAIA
                                                                                                                                                                                                                              DKNHPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVTIVLFVMATPE--TDK
                                                                                                                                                                                                                                                                                                              LADREGLVVIDETPAVGV---HLNFMATTGLGEGSERVSTWEKIRTFEHHODVLRELVSR
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TRDRKPKLAAHVFRERWINI 595
                                  TRDROPKLVAHVLRRLWSEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93; Mismatches 224;
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Best Local Simi
Matches 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel secreted form of Bacillus sp. betaglucuronidase (BoGUS). The microbial BoGUS polypeptide can be used as a reporter/effector molecule and as a diagnostic tool. The products of the invention can be used as markers for transgene constructions, e.g. in plants or insects. They can also be used for the cleavage and detoxification of glucuronides and to examine conjugation patterns of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wus; BOGUS; beta-glucuronidase; secreted; reporter molecule; receptor molecule; diagnostic tool; transgene construction; pinsect; cleavage; detoxification; glucuronide.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 618 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated microbial beta-glucuronidase
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LADRLGILVIDEAPHVGITRYHYN------PETQKIA-----EDNIRRMIDR
                                           KFLINNKPFYFKGFGKHEDTPINGRGFNEASNVMDFNILKWIGANSFRTAHYPYSEELMR
                                                          LRDGMNRVTVAVDNIL------DDSTLPVGLYSERHEEGLGKVIRNKPNFDFFNYA
                                                                                                                                                                                                                                                                         NHIGYVWYEREFTVPAYLKDQRİVLRFGSATHKAIVYVNGELVVEHKGGFLPFEAEINNS
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                                                                                                  GKVVASTEGLSGNVEIPNVILWEPLNTYLYQIKVELVNDGLTIDVYEEPFGVRTVEVNDG
                                                                                                                           KKIRTSNRFVEGEFILENARFWSLEDPYLYPLKVELEKDEYTLDI-----GIRTISWDEK
                                                                                                                                                         GLHRPVKIYTTPFTYVEDISVVTDFNGP---TGTVTYTVDFQ----GKAETVKVSVVDEE
                                                                                                                                                                                    GIIRPVLIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQEMTIKLG--EEE
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35.6%;
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Pred. No. 5.2e-67;
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       The present sequence is a microbial beta-glucuronidase (GUS) protein. GUS genes were obtained from six different genera: Enterobacter/Salmonella, CC genes were obtained from six different genera: Enterobacter/Salmonella, CC pseudomonas, Salmonella, Staphylococcus and Thermotoga. Microbial GUS can be used as a reporter/effector molecule for transgenic constructions and CC in in vitro diagnostic applications. It may also be used to generate constructions and CC sentinel plants that serve as bioindicators of environmental status. It may be used to generate transgenic insects for tracking insect CC populations or to facilitate the development of a bioassay for compounds that affect molecules critical for insect development (e.g. juvenile cC destined for release into the environment. In animal systems, secreted GUS may be used to achieve extracellular detoxification of glucuronides (e.g. toxin glucuronide) and to examine conjugation patterns of glucuronides. Microbial GUS may also be used in traditional medical consolutic assays, for drug testing, pharmacokinetic studies, following bioavailability studies, diagnosis of diseases and syndromes, following or consolution of disease or its response to therapy. Microbial GUS has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microbial; beta-glucoronidase; GUS; Enterobacter; Salmonella; Pseudomonas; Staphylococcus; Thermotoga; transgenic plant; bioindicator; transgenic insect; marker; glucuronide detoxification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel microbial beta-glucuronidase genes and gene products used as reporter/effector molecule, as diagnostic tool, in positive selection, target molecules to specific cells and to detect and track linked gene
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RESULT 10
AAB28409
ID AAB28
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AC AAB28
AC AAB28
DT 26-JA
DT Salmo
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KW Micro
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OS Salmo
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OS Salmo
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Salmonella

beta-glucoronidase

26-JAN-2001

(first

entry)

AAB28409

standard;

protein;

602

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WO200055333-A1

Microbial; beta-glucoronidase; GUS; Enterobacter; Salmonella; Pseudomonas; Staphylococcus; Thermotoga; transgenic plant; bioindicator; transgenic insect; marker; glucuronide detoxification.

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Best Local S
Matches 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       increased thermal stability, high turnover number and enzymatic activity. It is highly specific for the substrate and water soluble, and the substrates are stable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
584
                           547
                                                                                      487
                                                                                                                    467
                                                                                                                                               431
                                                                                                                                                                               409
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                                                                                                                                                                                                                                                           RLGILVIDEAPHVGITRYHYN-----
                                                                                                                                                                                                                                                                                                                   LNGKPVFLKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINANSFRTSHYPYSEEWLDLAD
:| || : ||||||| : |||| : |||| : ||||
                                                                                                                                                                                                                                                                                                                                                             VASTEGLSGNVEIPNVILWEPLNTYLYQIKVELVNDGLTIDVYEEPFGVRTVEVNDGKFL
                         ROPKLVAHVLRRLWSEV
                                                          DIDPVMETEE
                                                                                                                  LIDVIALNRYNGWYFDGGDLEAAKVHLR---QEFHAWNKRCPGKPIMITEYGADTVAGFH
                                                                                                                                              YFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHR----KPIFVTEFGADAIAGIH
                                                                                                                                                                                                        HPSVIMWSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDVALK
                                                                                                                                                                                                                                                                                                     INNKPFYFKGFGKHEDTPINGRGFNEASNVMDFNILKWIGANSFRTAHYPYSEELMRLAD
                                                                                                                                                                                                                                                                                                                                                                                RTSNRFVEGEFILENARFWSLEDPYLYPLKVELEKDEYTLDI-----GIRTISWDEKRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GMNRVTVAVDNIL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENELRVVVENRLKVGGFPSKVPDSGTHTVGFFGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYVWYEREFTVPAYLKDQRIVLRFGSATHKAIVYVNGELVVEHKGGFLPFEAEINNSLRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPFTYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTGKVKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQRNKKRFILILNGVWNLEV------TSKDRPIAVPGSWNE--QYQDLCYEE
                                                                                     YDPPOMFSEEYOAELVEKTIRLLLKKDYIIGTHVWAFADFKTPONVRRPILNHKGVFTRD
                                                                                                                                                                               HPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVTIVLFVMATPE--TDKVAE
                                                                                                                                                                                                                                         REGLVVIDETPAVGV---HLNFMATTGLGEGSERVSTWEKIRTFEHHQDVLRELVSRDKN
                                                                                                                                                                                                                                                                                                                                                                                                                      RPVKIYTTPFTYVEDISVVTDFNGP---TGTVTYTVDFQ----GKAETVKVSVVDEEGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPVLIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQEMTIKLG--EEEKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PINTETRGVFDLNGVWNFKLDYGKGLEEKWYESKLTDTISMAVPSSYNDIGVTKEIRNHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                          YQVEYYQANHVVFDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVFTRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.8%;
                           563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 925; DB 3; Pred. No. 1.1e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -DDSTLPVGLYSERHEEGLGKVIRNKPNFDFFNYAGLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                     ----PETOKIA-----EDNIRRMIDRHKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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Best Local Simi
Matches 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes were obtained from six different genera: Enterobacter/Salmonella, Staphylococcus and Thermotoga. Microbial GUS can be used as a reporter/effector molecule for transgenic constructions and in vitro diagnostic applications. It may also be used to generate serve as bioindicators of environmental status. It may be used to generate transgenic insects for tracking insect populations or to facilitate the development of a bioassay for compounds that affect molecules critical for insect development (e.g. juvenile commonne). Secreted GUS may also serve as a marker for beneficial fungical destined for release into the environment. In animal systems, secreted GUS may be used to achieve extracellular detoxification of glucuronides (e.g. toxin glucuronide) and to examine conjugation patterns of glucuronides. Microbial GUS may also be used in traditional medical diagnostic assays, for drug testing, pharmacokinetic studies, following progression of disease or its response to therapy. Microbial GUS has increased thermal stability, high turnover number and enzymatic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a microbial beta-glucuronidase (GUS) genes were obtained from six different genera: Enterobacter/s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel microbial beta-glucuronidase genes and gene products used as reporter/effector molecule, as diagnostic tool, in positive selection, target molecules to specific cells and to detect and track linked gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 602 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jefferson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             substrates are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CAMB-) CAMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is highly specific for the substrate and water
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                                    DEAPHVGI -----
                                                                                        LKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINANSFRTSHYPYSEEWLDLADRLGILVI
                                                                                                                                                         LYTTPKTFVEDITVVTQVAD---DLAQATVAWQVRANG---EVRVELRDAEQQLVASGQG
                                                                                                                                                                                                                                                                            LISAGESVRITVCVNNELNWQTIP-----PGVVTQGVNGKKQQAYFHDFFNYAGIHRSVM
                                                                                                                                                                                                                                                                                                               KVKSGEN-ELRVVVENRLKVGGFPSKVPDSGTHTVGFFGSFPPANF-DFFPYGGIIRPVL
                                                                                                                                                                                                                                                                                                                                                                                 CYBEGPFTYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGBKVGBNHIBYLPFEVDVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                MVRPQRNKKRFILILNGVWNLEVTSKD------RPIAVPGSWNEQY--QDL
                                                                   FTGFGRHEDADLRGKGFDNVLMVHDHALMDWIGANSYRTSHYPYAEEMLDWADEHGIVII
                                                                                                                                      EKGELLLEGPRLWQPGEGYLYELRVIAQHQDEQDEYPLRVGIRSVEVKGEQFLINHKPFY
                                                                                                                                                                                                                                                                                                                                                 RNYVGNVWYQREIRIPKGWDRQRIVLRFDAVTHYGKVWVNDQFLMEHQGGYTPFEADISH
DETAAVGFNLSLGISFDVGEKPKELYSDEAVNDETQRAHLQAIKELIARDKNHPSVVVVWS
                                                                                                                                                                                                                                         IEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQEMTIKLGEEEKKIRTSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                   MLRSVETATREIKKLDGLWSFCMDSEECGNAQQWWRQPLPQSRAIAVPGSYNDQFAAAEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.7%;
35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 920; DB 3;
Pred. No. 2.8e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 223;
                                -TRYHYNPETQKIAEDNIRRMIDRHKNHPSVIMWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             soluble, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein. GUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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 409
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RESULT 11
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                                                                                                                       Best Loc
Matches
                                                                                                                                               Query Match
                                                                                                                                                                                                         The present invention provides the protein and coding sequences Lactobacillus gasseri beta-glucuronidase (GUS). The protein has activity at acidic pHs, and thus can be used to detect low pH
                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid of Lactobacillus gasseri encoding beta glucuronidase having activity at acidic pH which is useful as repoprotein for highly aciduric organisms, or as marker of transformed
                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                          Claim 19; Page 49-51; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                        Russell WM,
                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta-glucuronidase; GUS; low pH; Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L gasseri beta-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM48998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM48998 standard; protein;
                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAL44836
                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAY-2001; 2001WO-US016667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactobacillus gasseri.
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                                                                                                                                                                                                                                                                                                                                                                                                 (UYNC-) UNIV
                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                2002-062529/08
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108 GE-NELRVVVENRLKVGGFP---SKVPDSGTHTVGFFGSFPPANFDFFPYGGIIRPVLIE 163
                                               48
                                                                                                                       207;
                        67
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                                                                                                                                    Similarity
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                       GDFWYQKDFFIPSFLKKKELYIRFGSVTHRAKVFINGHEVGQHEGGFLPFQVKISNYINY
                                             GPFTYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTGKVKS
                                                                                               PQRNKKRFILILNGVWNLEVT-----SKDRP----IAVPGSWNE--QYQDLCYEE
                                                                                                                                                                        598 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAWLDMYHRVFDRVSAVVGEQVWNFADFATSQGIMRVGGNKKGIFTRDRKFKSAAFLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRDRQPKLVAHVLR
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                                                                       PIQNKYRFNTLMNGTWQFETDPNSVGLDEGWNKELPDPEEMPVPGTFAELTTKRDRKYYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRYYGWYVQSGDLEKAEKVLEKELLAWQEKLHRPIIITEYGVDTLAGLHSMYNDMWSEEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRYYGWYIYQGRIEEGLQALEKDIEELYARHRKPIFVTEFGADAIAGIHYDPPQMFSEEY
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                NORTH CAROLINA STATE
                                                                                                                                                                                                                                                                                                                                                                        Klaenhammer
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                                                                                                                                                                                               present sequence
                                                                                                                                    30.6%;
34.1%;
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                                                                                                                                    Score 919.5; DE Pred. No. 3e-66;
                                                                                                                        Mismatches
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                                                                                                                                                                                                18
                                                                                                                                                                                             the protein
                                                                                                                                               DB 5;
                                                                                                                       227;
                                                                                                                       Indels
                                                                                                                                             Length
                                                                                                                                                598;
                                                                                                                       63;
                                                                                                                                                                                                                                                                                               reporter
                                                                                                                                                                                                                       maximum
                                                                                                                      Gaps
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RESULT 12
ADQ89612
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XX ADQ89
AC ADQ89
XX Antag
XX Cytos
KW Cytos
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Cytos
XX Droso
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   Claim 2;
                                                                 New cell cycle progression genes and proteins for modulating cell oprogression in cells, for preventing, treating or diagnosing cell proliferative diseases (e.g. cancer) or for identifying modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
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                                                                                                                                                                         WPI; 2004-544089/52.
N-PSDB; ADQ89611.
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06-MAY-2003; 2003US-0468402P
                                                                                                                                                                                                                                                                                                                                                                                                                         31-DEC-2003; 2003WO-GB005635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; cancer; cell
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Murine beta-glucuronidase

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a polynucleotide for preventing, treating or diagnosing a disease in an individual. The composition or the polypeptide, polynucleotide or RNA precursor, or antibody is useful for diagnosing, preventing or treating diseases (e.g. cell proliferative diseases such as cancer) in an individual. These may also be used for identifying substances capable of binding to or modulating the function of the polypeptide, capable of affecting the function of the corresponding gene, or capable of inhibiting the cell division cycle or cell cycle progression, preferably mitosis and/or meiosis. The present sequence represents an antagonist of cell cycle progression protein
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                                                                                                                                                                                                                                                                                           MLYPRESETREVRSLDGIWNFVRSDQANPTQGVRDEWYAKELSKSRPTIPMPVPASYNDI
QPKAAAHLLRK
                            QPKLVAHVLRR
                                                         YVWSEEFQTEVFSRHFKAFDELRKKGWFIGEFVWNFADFKTAQSYTRVGGNKKGVFTRAR
                                                                                   QMFSBEYQAELVEKTIRL---LLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRDR
                                                                                                                                   SVIMWSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVSMMDAPDERTRDVALKYFD
                                                                                                                                                                                                                                                                                                                      TLDIGIRTISWDEKRLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINANS
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                                                                                                                 IISFNRYNAWYSNAGRLD
                                                                                                                                                                                                                                  YRTSHYPYSEESMQFADEHGIMIIDECPSVDTE--NFSQELLGKHKSSLEQLIHRDRNHP
                                                                                                                                                                                                                                                              FRTSHYPYSEEWLDLADRLGILVIDEAPHVGITRYHYNPETQKIAEDNIRRMIDRHKNHP
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Matches 223
                                                                                                                                                                                                                                                                                                      therapeutic protein that can be encoded by an adeno-associated virus (AAV) vector of the invention. Such vectors comprise a promoter operably positioned upstream of a nucleic acid encoding a biologically-active therapeutic mammalian serpin or cytokine polypeptide, and optionally also include an enhancer sequence and a post-transcriptional regulatory sequence. A recombinant AAV virion comprising the vector, and a mammalian cell (preferably an endothelial, islet, hepatocyte, pancreas, kidney, muscle, spleen, liver, heart, lung, or brain cell) comprising the vector are claimed. A claimed composition comprises the vector, the recombinant AAV virion, AAV viral particles, or the mammalian cell, and is used in cancer, diabetes, autoimmune disease, pancreatic disease or liver disease therapy. The composition is also used in claimed methods for preventing type I diabetes, and for reducing the rate of disease progression of type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
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                                                                                                                                                                                                                                                                        Sequence 648 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New adeno-associated viral vector, useful in preparing a composition for treating or preventing e.g., cancer, diabetes, or autoimmune, pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Atkinson MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; beta-glucuronidase; gene therapy; cytostatic; antidiabetic; immunosuppressive; hepatotropic; adeno-associated virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; SEQ ID NO 23; 183pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-2002; 2002US-0374083P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of murine beta-glucuronidase precursor
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                                                           PPANFDFFPYGGIIRPVLIEFTDHARILDIWVDTSESEPEKKLGKVK--VKIEVSEEAVG
                                                                                                        LPFEVDVTGKVKSG---ENELRVVVENRLKVGGFPSKVP-----DSGTHTVGFFGSF
                                                                                                                              TQEAALRDFIGWVWYEREAILPRRWTQDTDMRVVLRINSAHYYAVVWVNGIHVVEHEGGH
                                                                                                                                                                             MLFPKESPSRELKALDGLWHFRADLSNNRLQGFEQQWYRQPLRESGPVLDMPVPSSFNDI
                                                                                                                                                                                                   MVRPQRNKKRFILILNGVWNLEV-TSKDR-------PIAVPGSWNEQ
                                   QDTSFDFFNYAGLHRSVVLYTTPTTYIDDITVITN---VEQDIGLVTYWISVQGSEHF--
                                                                                                                                                      YQDLCYEE--GPFTYKTTFYVPKXLSQ---KHIRLYFAAVNTDCEVFLNGEKVGENHIEY
                                                                                 LPFEADISKLVQSGPLTTCRITIAINNTLT----PHTLPPGTIVYKTDTSMYPKGYP--V
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                                                                                                                                                                                                                           Conservative
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/label= Beta-glucuronidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Song
                                                                                                                                                                                                                         Score 902.5; DB 7; Pred. No. 8.3e-65; 3; Mismatches 207;
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RESULT 14
AAE02444
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                                   Use of recombinant adeno-associated virus, comprising gene encoding protein defective or missing in lysosomal storage disease, in the manufacture of a medicament for treating the lysosomal storage disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine; adeno-associated viral expression vector; AAV; gene therapy; lysosomal storage disease; LSD; mucopolysaccharidoses VII; MPS VII; Sly syndrome; beta-glucuronidase; GUS; glycosaminoglycan; GAG.
 Disclosure;
                                                                                                                 N-PSDB; AAD06387.
                                                                                                                                                                                                             (AVIG-)
                                                                                                                                                                                                                                                                  17-NOV-1999;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
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                                                                                                                                   WPI; 2001-343814/36.
                                                                                                                                                                      Podsakoff G,
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Page 85-87;
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2000US-0215430P.
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                                                                                                                                                                        Watson G,
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27. .648
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97pp; English
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present invention relates to recombinant adeno-associated virus (AAV)

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RESULT 15
ABB70164
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AC ABB70
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                          Drosophila; developmental biology; cell signalling; insecticide;
                                                          Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression vectors and virions, which include genes coding for enzymes defective or missing in lysosomal storage disease (LSD). AAV is useful in the manufacture of a medicament for treating lysosomal storage disease e.g., mucopolysaccharidoses VII (MPS VII). MPS VII (Sly Syndrome) is due to the deficiency in the lysosomal enzyme beta-glucuronidase (GUS) which aids in the breakdown of glycosaminoglycans (GAGs). AAV is used in gene therapy. The present sequence is murine GUS protein. This sequence is
               pharmaceutical.
                                                                                                                                                         ABB70164 standard;
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Best Local Similarity
Matches 216; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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genes from Drosophila and
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Search Job tim	рь	γQ	Db	ş	Дb	ş
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## ALIGNMENTS

RESULT 1
A72300
beta-glucuronidase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Ju1-2004
C;Accession: A72300
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; RicC.M.

Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

Qy 361 NIRRMIDRHKNHPSVIMWSVANEPES	Qy 301 KDFNLLKWINANSFRTSHYPYSEEWI	QY 241 LYPLKVELEKDEYTLDIGIRTISWDE	Qy 181 EPEKKLGKVKVKIEVSEEAVGQEMTI	Qy 121 KVGGFPSKVPDSGTHTVGFFGSFPP;  Db 121 KVGGFPSKVPDSGTHTVGFFGSFPP;	Qy 61 XLSQKHIRLYFAAVNTDCEVFLNGER	Qy 1 MVRPQRNKKRFILILNGVWNLEVTSI Db 1 MVRPQRNKKRFILILNGVWNLEVTSI	Query Match 99.9%; Score Best Local Similarity 99.8%; Pred. Matches 562; Conservative 0; Mis	A; Status: preliminary A; Molecule type: DNA A; Residues: 1-563 <arn> A; Cross-references: UNIPROT:Q9X0F2; GB:? A; Experimental source: strain MSB8 C; Genetics: A; Genetics: A; Gene: TM1062 C; Superfamily: beta-glucuronidase</arn>	Nature 399, 323-329, 1999 A;Title: Evidence for lateral gene transfer between Archaea A;Reference number: A72200; MUID:99287316; PMID:10360571 A;Accession: A72300
NIRRMIDRHKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVSMMDAP 420	KDFNLLKWINANSFRTSHYPYSEEWLDLADRLGILVIDEAPHVGITRYHYNPETQKIAED 360 	LYPLKVELEKDEYTLDIGIRTISWDEKRLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMI 300 	EPEKKLGKVKVKIEVSEEAVGQEMTIKLGEEEKKIRTSNRFVEGEFILENARFWSLEDPY 240 	KVGGFPSKVPDSGTHTVGFFGSFPPANFDFFPYGGIIRPVLIEFTDHARILDIWVDTSES 180 	XLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTGKVKSGENELRVVVENRL 120 	MVRPQRNKKRFILILNGVWNLEVTSKDRPIAVPGSWNEQYQDLCYEEGPFTYKTTFYVPK 60 	Score 2999; DB 2; Length 563; Pred. No. 4.2e-197; 0; Mismatches 1; Indels 0; Gaps 0;	GB:AE001766; GB:AE000512; NID:g4981600; PIDN:AAD3614	sfer between Archaea and Bacteria from genome seq 16; PMID:10360571

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beta-glucuronidase (gusB) [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Cpate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C;Accession: C90485
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redd arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
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A; Residues: 1-570 < KUR>
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A; Accession: C90485
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                                                                                                                                                                                                               EFPVLGQGTFYPLMIKDFNLLKWINANSFRTSHYPYSEEWLDLADRLGILVIDEAP--HV 343
                                                                                                                                                                                                                                                                                ARFWSLEDPYLYPLKVELE-----KDEYTLDIGIRTISWDEKRLYLNGKPVFLKGFGKHE
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QALEKDIEELYARH-RKPIFVTEFGADAIAGIHYDPPQMFSEEYQAELVEKTIRLLLKKD
                                                                                                                                                                                   DFPILGKFTYGAVLVRDFYLMRKIGANSFRTSHYPYSNEHLDLADEMGFLVILEPPLCYS
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                                  IRREVELFKSLDSSRPVTFAS----HRSVRDLALEYVDVISLNYYHGWYTEWGDIDSGV
                                                                     FKALYETANEMDRTR PVVMVSMMDAPDERTRDVALKYFDIVCVNRYYGWYIYQGRIEEGL
                                                                                                           NISRVMSQEEIAKMFGDVKYFEKVRDTIKEMIRQHKNRPSVIMYSVMNEPPSDIREVAEF
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                                                                        A; Gene:
                                                                                         Genetics:
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N;Alternate names: beta-D-glucuronoside glucuronosohydrolase
C;Species: Mus musculus (house mouse)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 09-Jul-2004
C;Accession: A32576; B32576; T49692; A28954; A29977; A35798
R;Wawrzyniak, C.J.; Gallagher, P.M.; D'Amore, M.A.; Carter, J.B.; Lund, S.D.; Rinchik, Mol. Cell. Biol. 9, 4074-4078, 1989
A;Title: DNA determinants of structural and regulatory variation within the murine hara A;Reference number: A32576; MUID:89384641; PMID:2779578
A;Accession: A32576
A;Map position: 5
A;Introns: 70/3; 132/3; 193/2; 241/1; 303/3; C;Superfamily: beta-glucuronidase C;Keywords: glycosidase; hydrolase; lysosome
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A; Residues: 1-264, 'D', 266-319, 'V', 321-648 < DAM>
A; Residues: 1-264, 'D', 266-319, 'V', 321-648 < DAM>
A; Cross-references: GB: J02836; GB: J03035; GB: M20204; NID: g193716; PIDN: R; Gallagher, P.M.; D'Amore, M.A.; Lund, S.D.; Ganschow, R.E.
Genomics 2, 215-219, 1988
A; Title: The complete nucleotide sequence of murine beta-glucuronidase A; Reference number: A29977; MUID: 88284700; PMID: 3397060
A; Accession: A29977
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R; Funkenstein, B.; Leary, S.L.; Stein, J.C.; Catterall,
Mol. Cell. Biol. 8, 1160-1168, 1988
A; Title: Genomic organization and sequence of the Gus-s-
A; Reference number: 149692; MUID:88216590; PMID:2835664
A; Accession: 149692
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A;Molecule type: mRNA
A;Residues: 1-648 <WAW>
A;Cross-references: UNIPROT:P12265;
A;Cross-references: allele B
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-264, 'D', 266-319, 'V', 321-648 < GAL>
A; Residues: 1-264, 'D', 266-319, 'V', 321-648 < GAL>
A; Cross-references: GB: J03047; NID: g193522; PIDN: AAA37696.1; PIE
R; Li, H.; Takeuchi, K.H.; Manly, K.; Chapman, V.; Swank, R.T.
J. Biol. Chem. 265, 14732-14735, 1990
A; Title: The propeptide of beta-glucuronidase. Further evidence the serpin superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-232,'T',234-264,'D',266-319,'V',321-427,'K',429-615,'L',617-648
A;Cross-references: GB:M19279; NID:g193524; PIDN:AAA37697.1; PID:g309257
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A; Residues: 1-86,'I',88-648 <WA2>
A; Cross-references: GB: M28541; NID: G193720; PIDN: AAA63308.1;
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A; Residues: 593-648 <LIA>
A; Note: the location of the
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R;D'Amore, M.A.; Gallagher, P.M.; Korfhagen, T.R.; Ganschow,
Biochemistry 27, 7131-7140, 1988
                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: A35798; MUID:90368633; PMID:2394691
A;Accession: A35798
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                                                                                                                                                                                                                                  propeptide cleavage site a portion of this enzyme
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PMID:2835664
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PMID:2779578
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                                                                                411/2; 460/2; 488/3; 547/3; 593/1
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RESULT 4
A25047
beta-glucuronidase (EC 3.2.1.31) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A25047; S00345
R;Nishimura, Y.; Rosenfeld, M.G.; Kreibich, G.; Gubler, U.; Sabatini, D.D.;
Proc. Natl. Acad. Sci. U.S.A. 83, 7292-7296, 1986
A;Title: Nucleotide sequence of rat preputial gland beta-glucuronidase cDNA
A;Reference number: A25047; MUID:87016933; PMID:3463967
A;Accession: A25047
A;Accession: A25047
A;Accession: A25047
A;Cross-references: UNIPROT:P06760; GB:M13962; NID:g204329; PIDN:AAA41228.
A;Experimental source: female preputial gland
R;Powell, P.P.; Kyle, J.W.; Miller, R.D.; Pantano, J.; Grubb, J.H.; Sly, V
Biochem. J. 250, 547-555, 1988
A;Title: Rat liver beta-glucuronidase. cDNA cloning, sequence comparisons
**Deference number: S00345; MUID:88183378; PMID:335537
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RESULT 5
GBECGC
beta-glucuronidase (EC 3.2.1.31) uidA - Escherichia coli (strain K-12)
N;Alternate names: beta-D-glucuronoside glucuronosohydrolase; gusA protein
C;Species: Escherichia coli
C;Date: 30-Jun-1988 #sequence revision 05-Dec-1997 #text_change 09-Jul-200
C;Accession: C64918; I53717; Ā26487; S43555
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C64918
A;Status: nucleic acid sequence not shown; translation not shown
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A;Molecule type: mRNA
A;Residues: 'E',15-20,'L',22-486,'L',488-648 <POW>
A;Residues: 'E',15-20,'L',22-486,'L',488-648 <POW>
A;Cross-references: EMBL:Y00717; NID:g56270; PIDN:CAA68705.1;
C;Superfamily: beta-glucuronidase
C;Keywords: glycosidase; hydrolase
F;1-22/Domain: signal sequence #status predicted <MAT>
F;23-648/Product: beta-glucuronidase #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1,'V',3-603 <PUN>
A;Residues: 1,'V',3-603 <PUN>
A;Cross-references: EMBL:Z32701; NID:g475168; PID:g475169
C;Comment: This acid hydrolase catalyzes the cleavage of a wide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: S43555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, April 1994 A;Reference number: S43555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-419,'VHGNIS',427-603 <JEF>
A;Cross-references: GB:M14641; NID:g868017; PIDN:AAA68923.1; PID:g868020
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Best Local Sim
Matches 205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Gene: uidA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                      WSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVSMM--DAPDERTRDVALKYFDIV
                                                                                                                                                                              FYFTGFGRHEDADLRGKGFDNVLMVHDHALMDWIGANSYRTSHYPYAEEMLDWADEHGIV
                                                                                                                                                                                                     VLIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQEMTIKLGEEEKKIRTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 YVIAGKSVRITVCVNNELNWQTIPPGMVITDENGKKKQSYF-----HDFFNYAGIHRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVKSGEN-ELRVVVENRLKVGGFPSKV---PDSGTHTVGFFGSFPPANFDFFPYGGIIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVRPQRNKKRFILILNGVWNLEV------TSKDRPIAVPGSWNEQYQDLCY
                                                                                       VIDETAAVGFNLSLGIGFEAGNKPKELYSEEAVNGETQQAHLQAIKELIARDKNHPSVVM
                                                                                                                                                                                                                                                                     QGTSGTLQVVNPHLWQPGEGYLYELCVTAKSQTECDIYPLRVGIRSVAVKGEQFLINHKP
                                                                                                                                                                                                                                                                                                                                                        VMLYTTPNTWVDDITVVTHVAQ----DCNHASVDWQV----VANGDVSVELRDADQQVVATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNYAGNVWYQREVFIPKGWAGQRIVLRFDAVTHYGKVWVNNQEVMEHQGGYTPFEADVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EE--GPFTYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTG
WSIANEPDTRPQGAREYFAPLAEATRKLDPTRPITCVNVMFCDAHTDTISDL----FDVL
                                                                                                                                                                                                                                                                                                           RFVEGEFILENARFWSLEDPYLYPL----KVELEKDEYTLDIGIRTISWDEKRLYLNGKP
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A; Molecule type: mRNA
A; Residues: 520-585 < GUI>
A; Residues: 520-585 < GUI>
A; Cross-references: GB: M10618; NID: g183704; PIDN: AAA52621.1; PID: g183705
A; Cross-references: GB: M10618; NID: g183704; PIDN: AAA52621.1; PID: g183705
A; Tomatsu, S.; Fukuda, S.; Sukegawa, K.; Ikedo, Y.; Yamada, S.; Yamada, Nam. J. Hum. Genet. 48, 89-96, 1991
A; Title: Mucopolysaccharidosis type VII: characterization of mutations ar A; Title: number: A36538; MUID: 91090114; PMID: 1702266
A; Accession: A36538
                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:120025; OMIM:253220
A;Map position: 7q22-7q22
C;Superfamily: beta-glucuronidase
C;Keywords: glycoprotein; glycosidase; homotetramer; hydrolase; lysosome
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-651/Product: beta-glucuronidase, placental #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental source: placenta R;Shipley, J.M.; Miller, R.D.; Wu, B.M.; Grubb, J.H.; Christensen, S.G.; Kyle, J.W.; Genomics 10, 1009-1018, 1991
A;Title: Analysis of the 5' flanking region of the human beta-glucuronidase gene. A;Reference number: A40337; MUID:92009900; PMID:1916806
A;Accession: A40337
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C;Date: 05-Oct-1988 #sequence revision 05-Oct-1988 #text_change C;Accession: A26581; A40337; \( \bar{A}24983\); A36538
R;Oshima, A.; Kyle, J.W.; Miller, R.D.; Hoffmann, J.W.; Powell, Proc. Natl. Acad. Sci. U.S.A. 84, 685-689, 1987
A;Title: Cloning, sequencing, and expression of cDNA for human bA;Reference number: A26581; MUID:87118233; PMID:3468507
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A;Reference number: A24983; MUID:85232043; PMID:3924735
A;Accession: A24983
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A:Residues: 378-385,616-621,643-651 <TOM>
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A; Residues: 1-70 <SHI>
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A; Residues: 1-651 < OSH>
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    LPFEVDVTGKVKSG--ENELR--VVVENRLKVGGFPSKVP---
                                                 SODWRLRHFVGWVWYEREVILPERWTODLRTRVVLRIGSAHSYAIVWVNGVDTLEHEGGY
                                                                                                   YQD--LCYEEGPFTYKTTFYVPKXLSQ---KHIRLYFAAVNTDCEVFLNGEKVGENHIEY 94
                                                                                                                                                       MLYPQESPSRECKELDGLWSFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVPSSFNDI
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                                                                                                                                                                                                                                                                                   28.8%; Score 865.5; DB 2 34.5%; Pred. No. 2.8e-51;
                                                                                                                                                                                                                                                            105;
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                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                          DB 2;
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-DSGTHTVGFFGS 142
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RESULT 7

A85768

partial beta-D-glucuronidase [imported] - Escherichia coli (strain (c;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-0
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-0
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-0
C;Date: 16-Feb-2001 #text_change 09-0
C;Accession: A85768
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Pots
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Pots
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Pots
iller, L.; Grotbeck, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85768
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-368 <STO>
A;Cross-references: UNIPROT:Q8X671; GB:AE005174; NID:g12515602; PIDN
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
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HPDAEGFFKALYETANEMDRTRPVVMVSMM--DAPDERTRDVALKYFDIVCVNRYYGWYI
                                     NLSLGIGFEAGNKPKELYSEEAVNGETQQAHLQAIKELIARDKNHPSVVMWSIANEPDTR
                                                                                                               DADLRGKGFDNVLMVHDHALMDWIGANSYRTSHYPYAEEMLDWADEHGIVVIDETAAVGF
                                                                                                                                                                                        NPHLWQPGEGYLYELYVTAKSRTECDIYPLRVGIRSVAVKGEQFLINHKPFYFTGFGRHE
                                                                                                                                                                                                                          NARFWSLEDPYLYPL----KVELEKDEYTLDIGIRTISWDEKRLYLNGKPVFLKGFGKHE
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                                                                                                                                                                                                                                                                   Conservative
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                                                                        TRYHYNPETOKIAEDNIRRMIDRHKNHPSVIMWSVANEPESN
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Pred. No. 1e-39;
2; Mismatches 1
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Potamousis,
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K.; A
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A;Experimental source: strain O157:H7, substrain C;Genetics:
A;Gene: ECs2324
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A; Residues: 1-370 < HAY>
A; Cross-references: UNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: D90919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001
C;Accession: D90919
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.;
DNA Res. 8, 11-22, 2001
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                                                                                YQGRIEEGLQALEKDIEELYARHRKPIFVTEFGADAIAGIHYDPPQMFSEEYQAELVEKT
HRVFDRVSAVVGEQVWNFADFATSQGILRVGGNKKGIFTRDRKPKSAAFLLQKRWT
                     IRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRDRQPKLVAHVLRRLWS
                                                           QSGDLETAEKVLEKELLAWQEKLHQPIIITEYGVDTLAGLHSMYTDMWSEEYQCAWLDMY
                                                                                                                     PQGAREYFAPLAEATRKLDPTRPITCVNVMFCDAHTDTISDL----FDVLCLNRYYGWYV
                                                                                                                                                  HPDAEGFFKALYETANEMDRTRPVVMVSMM--DAPDERTRDVALKYFDIVCVNRYYGWYI
                                                                                                                                                                              NLSLGIGFEAGNKPKELYSEEAVNGETQQAHLQAIKELIARDKNHPSVVMWSIANEPDTR
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                                                                                                                                                                                                                                                                                                                                                                                 23.0%;
39.6%;
                                                                                                                                                                                                   62;
                                                                                                                                                                                                                                                                                                                                                             Score 691; DB
Pred. No. 1e-39
62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               691; DB 2;
No. 1e-39;
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Shiba, T.; Hattori, M
                                                                                                                                                                                                                                                                                                                                                                  125;
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RIMD 0509952
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                                                                                                                                                                                                                                                                                                                                                                                            Length 370,
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Shinagawa,
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                                                                                                                                                                                                                                                                                                                                                                 28;
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probable beta-galactosidase (EC 3.2.1.23) [imported] - Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Cpate: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004 C;Accession: D95842 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F. Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001 A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-f A;Reference number: A95842; MUID:21396508; PMID:11481431 A;Accession: D95842 A;Status: preliminary

N2-fixing

endo

F.J.;

Hernan

(strain

from

Clostridium

d

PID:g144839

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A; Molecule type: DNA
A; Residues: 1-755 < KUR>
A; Residues: 1-755 < KUR>
A; Cross-references: UNIPROT:Q92XF7; GB:AL591985; PIDN:CAC48404.1; PID:g15139876;
A; Cross-references: UNIPROT:Q92XF7; GB:AL591985; PIDN:CAC48404.1; PID:g15139876;
A; Experimental source: strain 1021, megaplasmid pSymB
R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; L.
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.;
A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Reference number: A96039; MUID:21368234; PMID:11474104
                                                        RESULT 10
JU0275
beta-galactosidase (EC 3.2.1.23) - Thermoanaerobacterium C;Species: Thermoanaerobacterium thermosulfurigenes C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_
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C;Superfamily: be
C;Keywords: glyco
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No. 2.5e-25;
                                                                                                                                                                                                   -HKDFGSGDRICYHGVMDMFREPKFAA
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  #text_change
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                                      thermosulfurigenes
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; Fisher, R.F.
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                                                        RESULT 11
D86872
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C;Superfamily: beta-galactosidase
C;Keywords: glycosidase; homodimer; hydrolase
F;389,429,462/Active site: Glu, Tyr, Glu #stat
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A; Mesidues: 1-716 <BUR>
A; Cross-references: UNIPROT: P26257;
A; Cross-references: Strain EM1
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R;Burchhardt, G.; Bahl, H.
Gene 106, 13-19, 1991
A;Title: Cloning and analysis of the beta-galactosidase-encoding
A;Reference number: JU0275; MUID:92039055; PMID:1840542
A;Accession: JU0275
  beta-galactosidase (EC 3.2.1.23) [imported] - Lacto C; Species: Lactococcus lactis subsp. lactis C; Date: 23-Mar-2001 #sequence_revision 23-Mar-2001
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Pred. No. 5e-25;
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                                      Lactococcus lactis subsp.
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    #text_change 03-Aug-2001
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C;Accession: D86872
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; We Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium L A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: D86872
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-996 <STO>
A;Cross-references: GB:AE005176; PID:g12725024; PIDN:AAK06078.1; GSP:A;Experimental source: strain IL1403
C;Genetics:
A;Gene: lacz
C;Superfamily: beta-galactosidase
C;Keywords: glycosidase; hydrolase
                   beta-galactosidase - Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11:
C;Accession: F72283
R;Nelson, K.E.; Clayton. R.A. Gill c b
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Best Local S
Matches 162
  ;Accession: F72283
;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
arrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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                                                                                                                                                                                                                                                                                                                                                               GYGSNH-----QALYDWCKSFDSSRPV----HYEGGDDASRG-ATDATDIICPMYARV
                                                                                                                                                                                                                                                                                                                                                                                                                                               RLGILVIDEA---PHVGIT---RYHYNPETQKIAEDNIRRMIDRHKNHPSVIMWSVANEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNGVWN-----LEVTSKDRPIAVPGSWNEQYQDLCYEEGPFTYKTTF----
                                                                                                                                                                                                  ILNHKGVFTRDRQPK
                                                                                                                                                                                                                                                                                                                                                                                              -- ESNHPDAEGFFKALYETANEMDRTRPVVMVSMMDAPDERTRDVALKYFDIVC-----
                                                                                                                                                                                                                                                                                                                                                                                                                             EYGLYVMDEANIETH-GMTPMNRLTNDPTYLPLMSERVTRMVMRDRNHPSIIIWSLGNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ECHGF-DAEIGVVNPKLWSDEIPYLYRLELTLMDRSGAVFHKETKKIGIRKIAIEKGQLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPVLIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQE-MTIKLGEEEKKIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPPYVPEANPVGAYSRYFDITKEWLESGHVHLTFEGVGSAFHFWLNGEYGGYSEDSRLPA
                                                                                                                                                                     SLN--GLVFPNRQAK
                                                                                                                                                                                                                                 ---FGKYWQA-----FREIDRLQGGFIWDWVDQGLLKDGNYAYGGDFGDKPNDRQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNGKPVFLKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINANSFRTSHYPYSEEWLDLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSVNLQWLPDNYLLDFSIKT---DLDEDLDFANVKLQAYAKNIDDACLEFKLYDDEQLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVDVTGKVKSGENELRVVVENRLKVGGFPSKVPDSGTHTVGFFGSFPPANFDFFPYGGII 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---YVPKX------LSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNGLWNFDHFSRISDVPKNWLELTESKTEIIVPSNWQIEFKD--KSDVPIYTNVTYPIPI
                                                                                                                                                                                                                                                               PQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAF-----ADFKTPQNVRRP
                                                                                                                                                                                                                                                                                                                               ---- VNRYYGWYIYQGRIEEGLQALEKDIEELYARHRKPIFVTEFGAD---AIAGIHYDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INGKALLVRGVNKHEFTPEHGYVVSEEVMIKDIKLMKEHNFNAVRCSHYPNDSRWYELCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSNRFVEGEFILENARFWSLEDPYLYPLKVELEK-----DEYTLDIGIRTISWDEKRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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26.3%;
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Pred. No. 8.7e-25;
1; Mismatches 209;
                                                 11-Jun-1999 #text_change
                                                                                    (strain MSB8)
                                                                                                                                                                                                                                                                                                -- VAGENRPLILCEYAHDMGNSLGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153;
                                                     21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactococcus
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                       Hickey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehrl
beta-galactosidase (EC 3.2.1.23) lacZ [validated] - Escherichia coli N;Alternate names: beta-D-galactosidase; lactase C;Species: Escherichia coli C;Date: 24-Apr-1984 #sequence revision 23-Sep-1997 #text change 09-Ju C;Accession: A90981; A92233; A93224; S06878; I41218; H64761; I40987; R;Kalnins, A.; Otto, K.; Ruther, U.; Muller-Hill, B. EMBO J. 2, 593-597, 1983
A;Title: Sequence of the lacZ gene of Escherichia coli.
                                                                                                                                   GBEC
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C; Genetics:
A; Gene: TM1193
C; Superfamily: }
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A;Title: Evidence for lateral gene transfer between Archaea A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72283
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1087 <ARN >
A;Residues: 1-1087 <ARN >
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Sim
Matches 163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQEMTIKLGEEEKK-----
GVVLPDRTPEPELYEVKKVYQNV
                                 GVFTRDRQPKLVAHVLRRLWSEV
                                                                        DYWDVIEKYPYLHGGCIWDWVDQGIR---
                                                                                                                                                                                  FDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYA--RHRKPIFVTEFG---ADAIAGI-
                                                                                                                                                                                                                                                           HPSVIMWSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVSMMDAPDERTRDVALKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LITPDGDEKTLVKETVKPEDRVLSFAFDVKDPKKWSAETPHLYVLKLKLGEDEKKVNFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLTDVLRPGKNLITVEV-----LKWSD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVTGKVKSGENELRVVVENRLKVGGFPSKVPDSGTHTVGFFGSFPPANFDFFPYGGIIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNGNWRFLFAKNPFEVPEDFFSEKFDDSNWDEIEVPSNWEMKGYGKPIYTNVVYPFEPNP 104
                                                                                                           -HYDPPQMFSEEYQA---ELVEKTIRLLLKKDYIIGTHVWAF-ADFKTPQNVRRPILNHK
                                                                                                                                                   VDVF------
                                                                                                                                                                                                                                                                                                 PNOTKWYDLCDYFGLYVIDEA-NIESHGIDWDPEVTLANRWEWEKAHFDRIKRMVERDKN
                                                                                                                                                                                                                                                                                                                                      PYSEEWLDLADRLGILVIDEAPHVGITRYHYNPET-----QKIAEDNIRRMIDRHKN
                                                                                                                                                                                                                                                                                                                                                                           RKIEIKDGTLLFNGKPLYIKGVNRHEFDPDRGHAVTVERMIQDIKLMKQHNINTVRTSHY
                                                                                                                                                                                                                                                                                                                                                                                                    RTISWDEKRLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINANSFRTSHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYLYALPKFHIRDVFVRTDLDENYRN-GKIFLDVEMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFVPKDDNPTGVYRRWIEIPEDWFKKEIFLHFEGVRSFFYLWVNGKKIGFSKDSCTPAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF-----TYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       beta-galactosidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -IRTSNRFVEGEFILENARFWSLEDPYLYPLKVELEKDEYTLDIGI
                                                                                                                                                                                                                        GDGVNFEKAAL-WIKKRDNTRLIHY-----EGTTRRGESYY
                                                                                                                                                 ----SLMYPKMDÍLLBÝÁSKKREKPFIMCÉYAHAMGNSVGNLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 452.5; DB 2
Pred. No. 9.4e-23;
7; Mismatches 222
                                  563
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09-Jul-2004 )987; A00898;

S14637;

S14

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A;Title: Three-dimensional structure of beta-galactosidase fro A;Reference number: A58594; MUID:94277211; PMID:8008071
A;Contents: annotation; X-ray crystallography, 2.50 angstroms R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; .A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12 A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64761
                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 2-1024 <FOW>
A; Residues: 2-1024 <FOW>
A; Note: this is the final paper in a series
R; Calos, M.P.; Miller, J.H.
Nature 285, 38-41, 1980
A; Title: Molecular consequences of deletion formation mediated
A; Reference number: A93224; MUID:80188189; PMID:6246435
A; Accession: A93224
                                                                                                                                                A; Acceptable type: DNA
A; Molecule type: DNA
A; Residues: 1-11, 43-50 < RES>
A; Residues: 1-11, 43-50 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 967-971, 'R', 973-1022, 'E', 1024 <MIK>
A; Residues: 967-971, 'R', 973-1022, 'E', 1024 <MIK>
A; Cross-references: GB: M38327; NID: g146061; PIDN: AAA23835.1; PID: g146062
R; Jacobson, R.H.; Zhang, X.; Dubose, R.F.; Matthews, B.W.
submitted to the Brookhaven Protein Data Bank, July 1994
A; Reference number: A65162; PDB: 1BGL
A; Contents: annotation; X-ray crystallography, 2.50 angstroms, residues 4
R; Jacobson, R.H.; Zhang, X.J.; DuBose, R.F.; Matthews, B.W.
Nature 369, 761-766, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X16313; NID:g41903; PIDN:CAA34380.1; PID:g41904 R;Mikryukov, N.N.; Petrov, N.A.; Karginov, V.A.; Vassilenko, S.K. Bioorg. Khim. 6, 1735-1736, 1980 A;Title: Nucleotide sequence of a lambda-plac 5-1 DNA region coding for A;Reference number: I41218 A;Accession: I41218
                                                                                                                                                                                                                                                 A;Title: Nucleotide sequence of the classical lacZ deletion delta A;Reference number: I40987; MUID:93083990; PMID:1339377 A;Accession: I40987
                                                                                                                                                                                                                                                                                                                                    R; Prentki, P. Gene 122, 231-232, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 356-476 < CAL>
R; Ruteshouser, E.C.; Richardson, J.P.
J. Mol. Biol. 208, 23-43, 1989
A; Title: Identification and characterization of transcription A; Reference number: S06878; MUID:89362462; PMID:2475637
A; Accession: S06878
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A;Title: Amino acid sequence of beta-galactosidase. XI.
A;Reference number: A92233; MUID:78218239; PMID:97298
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A;Cross-references: UNIPROT:P00722; GB:V00296; NID:g41901;
A;Note: translation of initiator Met is not shown
R;Fowler, A.V.; Zabin, I.
  A; Description:
                                                                                   A; Map position: 8 min
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J. Biol. Chem. 2
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A; Molecule type: 1
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A; Residues: 1-147 < RUT>
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                               Function
                                                                                                                                         Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: nucleic acid sequence not shown; translation not shown
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  catalyzes
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  hydrolysis of lactose
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                                                                                                                                                                  NID: 940882;
                                                                                                                                                                    PIDN: CAA41206.1;
into
galactose
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and glucose
                                                                                                                                                                PID:g40883
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C;Superfamily: beta-galactosidase
C;Keywords: glycosidase; homotetramer; hydrolase; magnesium
F;2-1024/Product: beta-galactosidase #status experimental <MAT>
F;2-50/Region: alpha complementation
F;51-218/Domain: 1, jelly-roll beta-barrel #status predicted <DM1>
F;219-334/Domain: 2, fibronectin type-III fold #status predicted <DM2>
F;335-627/Domain: 3, distorted TIM barrel #status predicted <DM3>
F;628-737/Domain: 4, fibronectin type-III fold #status predicted <DM4>
F;738-1024/Domain: 5, anti-parallel beta-sandwich #status predicted <DM5>
F;417,419,462/Binding site: magnesium (Glu, His, Glu) #status experimental
F;462,504,538/Active site: Glu, Tyr, Glu #status predicted
                                                                                                                                                                                                                                                             R;hayasıı, ...
gasawara, N.; Yasunaga, T.; Kuhara, S.; C.......
DNA Res. 8, 11-22, 2001
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
                                                                                                                                                 A;Status: procession A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1024 < HAY>
A; Residues: 1-1024 < HAY>
A; Cross-references: UNIPROT: Q8X685; GB: BA000007;
A; Cross-references: strain O157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                            beta-D-galactosidase [imported] - Escherichia coli C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 C;Accession: E90678
                                                                                             A;Gene: ECs0397
C;Superfamily: beta-galactosidase
                                                                                                                                                                                                                                                                                                                                                                      R;Hayashi,
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Best Local Similarity
Matches 132; Conserv
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Local 5.
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                                                                                                                                                                                                                                                                                                                                                T.; Makino, K.; Ohnishi,
N.; Yasunaga, T.; Kuhara,
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                h 13.5%;
Similarity 25.2%;
59; Conservative E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNGVWNLEVTSKDRPIAVPGSWNE-------
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                Score 405.5; DE
Pred. No. 1.4e-1
8; Mismatches 2
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Shiba, T.; Hattori,
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                                          DB 2;
le-19;
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RIMD 0509952
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                                                       Length
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                                                                                                                                                                                                                                                                                                                                                  ; Yokoyama, K.;
Shinagawa, H.
                                                                                                                                                                                   PID:g13359854; GSPDB:
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169;

Gaps

26;

VPSNWQMHGYDAPIYTNVP1TVNP 112  VNTDCEVFLNGEKVGENHIEYLPFEV 99    : :	Ş	Query Ma Best Loo Matches	A;Statu A;Molec A;Resid A;Cross A;Exper C;Genet A;Gene:C;Super	R;Perna iller, Nature Nature A;Title A;Refer A;Acces	RESULT A85529 beta-D- C;Speci C;Date: C;Acces	용	ş	Db S	<b>§</b>	\$ 5	₽.	<b>9</b> 5	g 6	g 4	Db	δ	B <b>2</b>	? 8	\$	DЪ	8	Db	ई
B. C. F.	5 LNGVWNLEVTSKDRPIAVPGSWNEG 4	atch 13.5%; Score 405.5; DB 2; Length 1024; cal Similarity 25.2%; Pred. No. 1.4e-19; 159; Conservative 88; Mismatches 216; Indels 169; Gaps 26	8X685; GB:AE005174; NID:g12513175; PIDN:AAG54693. 0157:H7, substrain EDL933	G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J. vis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; nterohemorrhagic Escherichia coli O157:H7.	d] - Escherichia coli (strain O157:H7, substrain _revision 16-Feb-2001 #text_change 09-Jul-2004	85 PWSAYGGDFGDTPNDRQFCMNGLVFADRTP	20 VWAFADEKTPQNVRRPILNHKGVFTRDRQP	: ::      :: :    ::    ::  :   ::  :   ::  :   ::  :   ::  :   ::  :   ::  :	EFGADAIAGIHYDPPOMFSEEYOAELVEKTIRLLLKKDYIIGTH 5	MMDAPDERTRDVALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHRKPIFVT 4	:  :    :   :         : :	UHPSVIMMSVANEPESNHPDAEGFEKALYETANEMDETEDVVMVS	TSHYPYSEEWLDLADRLGILVIDEAPHVGITRYHYNPETQKIAEDNIRRMIDRHK	56 DIGIRTISWDEKRLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINANSFR   :	SGTAPFGGEIIDERGGYADRVTLGLNVENPKLWSAEIPNIYRAVVELHTADGTLIEAEAC 3	TSNRFVEGEFI	VSLLHKPTTQISDFHVATLFNDDFSRAVLEAEVQMYGELRDELRVTVSLWQGETQVA	DLSAFLRAGENRLAVMV-LRWSDGSYLEDQDMWRMSGIFRD	DVTGKVKSGENELRVVVENRLKVGGFPSKVPDSGTHTVGFFGSFPPANFDFFPYGGIIRP 1	PFVPTENPTGCYSLTFNVDESWLQEGQTRIIFDGVNSAFHLWCNGRWVGYGQDSRLLSEF	PFTYKTTFYVPKX-LSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEV	5 LNGEWQFVWFPAPEAVPESWLECDLPDADTVVVPSNWQMHGYDAPIYTNVTYPITVNP	15 LNGVWNLEVTSKDRPIAVPGSWNE

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                                        520 VWAF--ADEKTPONVRRPILNHKGVFTRDROP 549
                                                                                                                                                                                                                                                         450 NHPSVIIWSLGNESGHGANH------DALYRWIKSVDPSRPVQYEGGGADTSATDIICP 502
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                                                                                                          EFG---ADAIAGIHYDPPQMFSEEYQA------ELVEKTIRLLLKKDYIIGTH
                                                                                                                                                                                                            MMDAPDERTRDVALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHRKPIFVT 475
                                                                                                                                                                                                                                                                                NHPSVIMWSVANEP--ESNHPDAEGFFKALYETANEMDRTRPV------VMVS
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PWSAYGGDFGDTPNDRQFCMN--GLVFADRTP 614
                                                                                   EYAHAMGNSLGG-----FAKYWQAFRQYPRLQGGFVWDLVDQS---LIKYDE--NGN 584
                                                                                                                                                                     MYARVDEDQPFPAVPKWSI-----KKWLSLPGEM------RPLILC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLIEFTDHARILDIWVDTSESEPEKKL---GKVKVKIEVSEEAVGQEMTIKLGEEEKKIR 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFVPTENPTGCYSLTFNVDESWLQEGQTRIIFDGVNSAFHLWCNGRWVGYGQDSRLLSEF 172
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Search completed: September 1, 2005, 19:33:26
Job time : 45 secs

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1628.817 Million cell updates/sec
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  GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Q8E0N2
Q7UCE6
Q83RC5
Q7PZE2
Q8X671
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BGLR_MOUSE
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Q97UI1
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Q97ui1 sulfolobus
Q8xp19 clostridium
Q8xp14 clostridium
Q9afa2 staphylococ
Q9ahj8 lactobacill
Q6nl66 drosophila
Q9v8r0 drosophila
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Q9v8r0 mus musculu
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018835
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Q9ahj4
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                                                                                                                                   0 rattus norv
5 canis famil
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5 cercopithec
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c canorhabdi
7 ruminococcu
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9 drosophila
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InterPro; IPR006101; Glyco_hydro_21.

InterPro; IPR006102; Glyco_hydro_25B.

InterPro; IPR006104; Glyco_hydro_25B.

InterPro; IPR006103; Glyco_hydro_27IM.

Pfam; PF00703; Glyco_hydro_2; 1.

Pfam; PF02836; Glyco_hydro_2_C; 1.
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01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Beta-glucuronidase (GusB) (EC 3.2.1.31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=gusB; OrderedLocusNames=SSO3036;
Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sulfolobus
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                                                                                               MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799; Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaer
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Complete proteome; Glycosidase;
SEQUENCE 570 AA; 66795 MW; I
flesh-eater.";
Proc. Natl. Acad. Sci. U.S..
EMBL; AP003185; BAB79853.1;
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2; Mismatches 191;
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Pfam; PF00703; Glyco_hydro_2; 1.
Pfam; PF02836; Glyco_hydro_2 C; 1.
Pfam; PF02837; Glyco_hydro_2 N; 1.
PRINTS; PR00132; GLHYDRLASE2.
PROSITE; PS00608; GLYCOSYL_HYDROL_F2_1; 1.
PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; UNKNOWN_1.
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                                                                Clostridia;
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Matches 226
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GO; GO:0004553; F:hydrolase activity, hydrolyzing O-9

GO; GO:0005975; P:carbohydrate metabolism; IEA.

Pfam; PF00703; Glyco_hydro_2; 1.

Pfam; PF02836; Glyco_hydro_2_C; 1.

Pfam; PF02837; Glyco_hydro_2_N; 1.

PFAM; PF02837; Glyco_hydro_2_N; 1.

PRINTS; PR00132; GLHYDRLASE2.

PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.

PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; UNKNOWN 1.

PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; UNKNOWN 1.

PROSITE; PS00608; GLYCOSYL_HYDROL_F2_3; UNKNOWN 1.

PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; UNKNOWN 1.
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SEQUENCE FROM
STRAIN=13;
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DOI=10.1128/JB.184.9.2333-2343.2002;
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                 QPKLVAHVLRRLWSEV
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Matches 221
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GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR008979; Gal bind like.

InterPro; IPR006101; Glyco hydro 2:

InterPro; IPR006104; Glyco hydro 2:B.

InterPro; IPR006103; Glyco hydro 2:TIM.

Pfam; PF00703; Glyco hydro 2:TIM.

Pfam; PF02836; Glyco hydro 2:C; 1.

Pfam; PF02836; Glyco hydro 2:C; 1.

Pfam; PF02837; Glyco hydro 2:N; 1.

PFO0837; Glyco hydro 2:N; 1.

PROSITE; PS00132; GLHYDRLASE2.

PROSITE; PS00132; GLYCOSYL HYDROL F2 1; 1.

PROSITE; PS00608; GLYCOSYL HYDROL F2 2; 1.

PROSITE; PS00608; GLYCOSYL HYDROL F2 2; 1.

PROSITE; PS00608; GLYCOSYL HYDROL F2 2; 1.
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HSSP; P08236; 1BHG.
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01-JUN-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Submitted (FEB-2001)
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Bacteria; Firmicutes; Bacillales;
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NHIGYVWYEREFTVPAYLKDQRÍVLRFGSATHKAIVYVNGELVVEHKGGFLPFEAEINNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YEEGPFTYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTGK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MLYPINTETRGVFDLNGVWNFKLDYGKGLEEKWYESKLTDTISMAVPSSYNDIGVTKEIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001) to the AAK29422.1;
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35.6%;
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17,
25,
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EMBL/GenBank/DDBJ
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Last sequence
Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 929; DB 2;
Pred. No. 1.3e-52;
3; Mismatches 224
                                                                                                                                                                         HLNFMATTGLGEGSERVSTWEKIRTFEHHODVLRELVSR
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-KPIFVTEFGADAIA
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                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 207
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REMBL; AF305888; AAK07836.1; -.

RHSSP; P08236; 1BHG.

GO; GO:0004553; F:hydrolase activity, hydrolyzing O-g
GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR008979; Gal bind like.

InterPro; IPR006101; Glyco_hydro_21g.

InterPro; IPR006102; Glyco_hydro_21g.

InterPro; IPR006104; Glyco_hydro_22B.

InterPro; IPR006104; Glyco_hydro_27IM.

R InterPro; IPR006103; Glyco_hydro_27IM.

R Pfam; PF00703; Glyco_hydro_2; 1.

R Pfam; PF02836; Glyco_hydro_2 C; 1.

Pfam; PF02837; Glyco_hydro_2 C; 1.

R Pfam; PF02837; Glyco_hydro_2 N; 1.

R PF1STS; PR00132; GLHYDRIASE2.

R PROSITE; PS00719; GLYCOSYL HYDROL F2 1; 1.

R SEQUENCE 598 AA; 69762 MW; 5398F060B2DD887D CRC6/
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01-JUN-2001
01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Russell W.M., Klaenhammer T.R.;
"Identification and cloning of gusA, encodin from Lactobacillus gasseri ADH.";
Appl. Environ. Microbiol. 67:1253-1261(2001)
EMBL; AF305888; AAK07836.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes;
Lactobacillus.
NCBI_TaxID=1596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21141841; PubMed=11229918;
DOI=10.1128/AEM.67.3.1253-1261.2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta-glucuronidase.
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                                                                                                                                                                                                                                                                                             Similarity
TSSLTIKNPHLWSPNDPYSYKIKIEMLEDGKTVDEYTDKIGIRTVKIVNDKILLNNHPIY
                                                                                                                                      GE-NELRVVVENRLKVGGFP---SKVPDSGTHTVGFFGSFPPANFDFFPYGGIIRPVLIE
                                                                                                                                                                                 GPFTYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTGKVKS
                                                                                                                                                                                                                                       PQRNKKRFILILNGVWNLEVT-----SKDRP----IAVPGSWNE--QYQDLCYEE
                       EGEFILENARFWSLEDPYLYPLKVELEK----DEYTLDIGIRTISWDEKRLYLNGKPVF
                                                                              FTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEFAVGQ-EMTIKLGEEEKKIRTSNRFV
                                                                                                           DQTNRVTVLVNNELSEKAIPCGTEEILDNGQ-----KLAQPYFDFFNYSGIMRNVWLL
                                                                                                                                                                 GDFWYQKDFFIPSFLKKKELYIRFGSVTHRAKVFINGHEVGQHEGGFLPFQVKISNYINY
                                                                                                                                                                                                                        PIQNKYRENTLMNGTWQFETDPNSVGLDEGWNKELPDPEEMPVPGTFAELTTKRDRKYYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIHYDPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAELIDVIALNRYNGWYFDGGDLEAAKVHLR---QEFHAWNKRCPGKPIMITEYGADTVA
                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                            30.6%;
34.1%;
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17,
25,
                                                                                                                                                                                                                                                                              110;
                                                                                                                                                                                                                                                                             Score 919.5; DE
Pred. No. 5.6e-5
LO; Mismatches 2
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Last annotation update)
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                                                    YQLANNKAT I TYN I BANNNAB FKVTL FDNQKEVACATSKN
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6e-52;
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                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                         598;
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207 222 152 167

253 281

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Query Match
Best Local S
Matches 212
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A Park S., Wan K., Yu C., Rubin G.M., Celniker S.;

L Submitted (APR-2004) to the EMBL/GenBank/DDBJ datak

EMBL; BT012475; AAS93746.1; -.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R InterPro; IPR008979; Gal bind like.

InterPro; IPR006101; Glyco_hydro_21g.

R InterPro; IPR006102; Glyco_hydro_22B.

R InterPro; IPR006104; Glyco_hydro_2SB.

InterPro; IPR006103; Glyco_hydro_2SB.

InterPro; IPR006103; Glyco_hydro_2TIM.

R InterPro; IPR006025; Pept M Zn BS.

R InterPro; IPR006025; Pept M Zn BS.

R Pfam; PF02836; Glyco_hydro_2 C; 1.

R Pfam; PF02837; Glyco_hydro_2 N; 1.

R PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.

R PROSITE; PS00608; GLYCOSYL_HYDROL_F2_1; 1.

R PROSITE; PS00608; GLYCOSYL_HYDROL_F2_1; 1.

R PROSITE; PS00608; GLYCOSYL_HYDROL_F2_1; 1.

R PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.

SEQUENCE 670 AA; 77050 MW; 00AE0E67AEID9E8C CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
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                                                                                                                                                                                                                                Similarity
               YQD-LCYEEGPFTYKTTFYVPKXLSQ-KHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPF
                                                                                            MLYPRESETREVRSLDGIWNFVRSDQANPTQGVRDEWYAKELSKSRPTIPMPVPASYNDI
                                                                                                                                                  MVRPQRNKKRFILILNGVWNL-----
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WEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., A Sutton G.G., Wortman J.R., Andell M.D., Zhang Q., Chen L.X., A Sutton G.G., Wortman J.R., Andell M.D., Zhang Q., Chen L.X., A Sutton G.G., Wolson C.R., Gabor G.L., A Handell J., Andrews-Pfannkoch C.R., Gabor G.L., A Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., A Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., A Bartis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., A Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., A Boblos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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OT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update
OT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update
E CG15117-PA (LD04718p).
N ORFNames=CG15117;
S Drosophila melanogaster (Fruit fly).
S Eukaryota; Metazoa; Arthropoda; Hexapoda; Insection Neoptera; Endopterygota; Diptera; Brachycera; Mui Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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InterPro; IPR008101; Glyco hydro 2.
InterPro; IPR008102; Glyco hydro 21g.
InterPro; IPR008104; Glyco hydro 2SB.
InterPro; IPR008103; Glyco hydro 2TIM.
InterPro; IPR0080103; Glyco hydro 2TIM.
InterPro; IPR008025; Pept M Zn BS.
Pfam; PF00703; Glyco hydro 2; I.
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FlyBarolyzing O-glycosyl GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl GO; GO:0005975; P:carbohydrate metabolism; IEA.

GO; GO:0005979; Gal bind_like.
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HSSP; P08236; 1
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; PS00719; GLYCOSYL_HYDROL_F2_1; 1.

; PS00608; GLYCOSYL_HYDROL_F2_2; 1.

; PS00142; ZINC_PROTEASE; UNKNOWN_1.

E 656 AA; 75166 MW; 34168D33C8F88A20
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Kaminker J.S., Bergman C.M., Kronmiller
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Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Patel S., Frise E., Wheeler D.A., Lewis S.E.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila
a genomics perspective.";
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                          melanogaster euchromatin
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Zhu X., Smith H.O.
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R HSSP; FUBLIS, LEWING.
R FlyBase; FBgn0034417; CG15117.
R GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .;
R GO; GO:0005975; P:carbohydrate metabolism; IEA.
)R InterPro; IPR008979; Gal_bind like.
)R InterPro; IPR006101; Glyco_hydro_2:
)R InterPro; IPR006102; Glyco_hydro_2:
)R InterPro; IPR006104; Glyco_hydro_2SB.
InterPro; IPR006103; Glyco_hydro_2TIM.
DR InterPro; IPR006025; Pept M Zn BS.
DR Pfam; PF02836; Glyco_hydro_2 C; 1.
DR Pfam; PF02836; Glyco_hydro_2 C; 1.
DR Pfam; PF02836; Glyco_hydro_2 N; 1.
DR Pfam; PF02837; Glyco_hydro_2 N; 1.
DR PROSITE; PS00132; GLHYDRLASE2
DR PROSITE; PS00142; ZINC_PROTEASE; ÜNKNOWN 1.
SEQUENCE 670 AA; 77036 MW; 7A9F23351E458C90 CRC64;
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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SVIMWSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVSMMDAPDERTRDVALKYFD
                            YRTSHYPYSEESMQFADEHGIMIIDECPSVDTE--NFSQELLGKHKSSLEQLIHRDRNHP
                                                                                         LYDKDGILVANATSDQKLGGKLQVNPVKPWWPYLMHSEPGYLYQLEIKLLATNDELLDVY
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                                                       FRTSHYPYSEEWLDLADRLGILVIDEAPHVGITRYHYNPETQKIAEDNIRRMIDRHKNHP
                                                                                                                       TLDIGIRTISWDEKRLYLNGKPVFLKGFGKHEEFPVLGQGTFYPLMIKDFNLLKWINANS
                                                                                                                                                                                    LGEEEKKI----RTSNRFVEGEFILENARFW-----SLEDPYLYPLKVELEK-----DEY
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RESULT 10
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ID BGLR MOUSE
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STRAIN=C3H/HeJ, and YBR; TISSUE=Sperm;

MEDLINE=89384641; PubMed=2779578;

Wawrzyniak C.J., Gallagher P.M., D'Amore M.A.,

Wawrzyniak C.J., Ganschow R.E.;
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MEDLINE=88284700; PubMed=3397060;
Gallagher P.M., D'Amore M.A., Lund S.
"The complete nucleotide sequence of and its deduced polypeptide.";
Genomics 2:215-219(1988).
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=89062453; PubMed=3196706;
D'Amore M.A., Gallagher P.M., Kor
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01-OCT-1989 (Rel. 12, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Beta-glucuronidase precursor (EC 3.2.1.31).
                                                                                                               Funkenstein B., Leary S.L., Stein conference organization and sequence murine beta-glucuronidase gene.";
                                                                                                                                                                                SEQUENCE FROM N.A.
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Mus musculus (Mouse).
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01-OCT-1989 (Re
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Mammalia; Eutheria;
                                                                                                                                                               MEDLINE=88216590; PubMed=2835664;
                                                                                                                                                                                                              "DNA determinants of structural and regulatory murine beta-glucuronidase gene complex."; Mol. Cell. Biol. 9:4074-4078(1989).
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                                                                                                                                                                                                                                                                                                                                                                                              'Complete
                                              . Cell. Biol. 8:1160-1168(1988 FUNCTION: Plays an important and keratan sulfates. CATALYTIC ACTIVITY: A beta-D-
D-glucuronate.
SUBUNIT: Homotetramer.
SUBCELLULAR LOCATION:
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   LOCATION: Lysosomal.
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InterPro; IPR006101; Glyco_hydro_2.
InterPro; IPR006102; Glyco_hydro_21g.
InterPro; IPR006104; Glyco_hydro_2SB.
InterPro; IPR006103; Glyco_hydro_2TIM.
Pfam; PF00703; Glyco_hydro_2TIM.
Pfam; PF02836; Glyco_hydro_2; 1.
Pfam; PF02837; Glyco_hydro_2_C; 1.
Pfam; PF02837; Glyco_hydro_2_N; 1.
Pfnm; PF02837; Glyco_hydro_2_N; 1.
PfnNTS; PR00132; GLHYDRLASE2.
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EMBL; J02836; AAA98623.1; -.
EMBL; M63836; AAA63309.1; -.
EMBL; M28540; AAA63307.1; -.
EMBL; M28541; AAA63308.1; -.
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PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.

PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.

PROSITE; PS00608; GLYCOSIdase; Hydrolase; Lyso
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SEQUENCE:
STRAIN=NMRI; Troccet;
Director MGC Project;
Submitted (JUN-2004) to the EMBL/Genbaux, Submitted (JUN-2004) to the EMBL/Genbaux, Submitted (JUN-2004) to the EMBL/Genbaux, Submitted (JUN-2004) to the EMBL/Genbaux, Submitted (JUN-2004) to the EMBL/Genbaux, Submitted (JUN-2004) to the EMBL, BC071226; F:hydrolase activity, hydrolyz DR GO; GO:0005975; P:carbohydrate metabolism; IEJ DR InterPro; IPR008101; Gal_bind_like.

DR InterPro; IPR006101; Glyco_hydro_2.

Therefore: IPR006102; Glyco_hydro_21g.

Therefore: IPR006104; Glyco_hydro_22B.
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                                                                                                                                                                                                                                                                                                                   "Generation and initial analysis and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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Rodentia;
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Last sequence update)
Last annotation update)
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RESULT 12
BGLR FELCA
ID BGLR FELCA STANDARD; PRT; 6
AC 097524;
DT 15-JUL-1999 (Rel. 38, Created)
DT 25-OCT-2004 (Rel. 45, Last annotation)
DE Beta-glucuronidase precursor (EC 3.2.1
GN Name=GUSB;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata
OC Mammalia; Eutheria; Carnivora; Fissipelox
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT MPS VI
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Best Local S
Matches 224
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Pfam; PF00703; Glyco hydro 2; 1.

Pfam; PF02836; Glyco hydro 2 C; 1.

Pfam; PF02837; Glyco hydro 2 N; 1.

Pfam; PF02837; Glyco hydro 2 N; 1.

PRINTS; PR00132; GLHYDRLASE2.

PROSITE; PS00719; GLYCOSYL HYDROL F2 1; 1.

PROSITE; PS00608; GLYCOSYL HYDROL F2 1; 1.

SEQUENCE 648 AA; 74195 MW; CCD8F84C3CD6C498
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                                                                                                                                                                                                                                                           NKKGIFTRQRQPKTSAFILRERYW
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35.9%;
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Craniata; Vertebrata; ; Fissipedia; Felidae;

Euteleostomi; Felis.

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InterPro; IPR008101; Glyco hydro_2.
InterPro; IPR006101; Glyco_hydro_21g.
InterPro; IPR006102; Glyco_hydro_22g.
InterPro; IPR006104; Glyco_hydro_2SB.
InterPro; IPR006103; Glyco_hydro_2TIM.
Pfam; PF00703; Glyco_hydro_2; 1.
Pfam; PF02836; Glyco_hydro_2; 1.
Pfam; PF02837; Glyco_hydro_2 C; 1.
Pfam; PF02837; Glyco_hydro_2 N; 1.
PRINTS; PR00132; GLYCORY, EVERONE PRO0132; GLYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.ish-sik-kicensersed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disease
Signal.
SIGNAL
CHAIN
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT SITE CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 58:121-128(1999).
-!- FUNCTION: Plays an important role and keratan sulfates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
MEDLINE=99296826; PubMed=10366443; DOI=10.1006/geno.1999.5825;
Fyfe J.C., Kurzhals R.L., Lassaline M.E., Henthorn P.S., Alur 1
Wang P., Wolfe J.H., Giger U., Haskins M.E., Patterson D.F., Su
Jain S., Yuhki N.;
"Molecular basis of feline beta-glucuronidase deficiency: an au
model of mucopolysaccharidosis VII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF012423; AAD01498.1; -. EMBL; AF012424; AAD01499.1; -. HSSP; P08236; 1BHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the glycosyl hydrolase 2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISEASE: Defects in GUSB are the type VII (MPS VII), an inherited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Homotetramer (By similarity) SUBCELLULAR LOCATION: Lysosomal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: A beta-D-glucuronoside
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PS00608; GLYCOSYL_HYDROL_F2_2; 1.
mutation; Glycoprotein; Glycosidase;
                                                                                                                                                                          EVDVTGKVKSG---ENELRVVVENRLKVGGFPSKVP-----DSGTHTVGFFGSFPPA
 KLGEEEKKIRTSNRFVEGEFILENARFW----SLEDP-YLYPLKVELE----
                                       NFDFFNYAGLHRPVLLYTTPTTYIDDITISTSVNQ-DTGLVDYQIFVEGGEHF----QLEV
                                                                                    NFDFFPYGGIIRPVLIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQEMTI
                                                                                                                               EADISKLVQSGPLASCRITIAINNTLT----PHTLPPGTILYQTDTSKYPKGYF--VQNI
                                                                                                                                                                                                                      RQLRSFVGWVWYEREATLPQRWTQDLGTRVVLRIGSAHYYAIVWVNGVHVAEHEGGHLPF
                                                                                                                                                                                                                                                                   --LCYEEGPFTYKTTFYVPKXLSQ---KHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPF
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Proton donor (By similarity N-linked (GlcNAc. . .) (Pot N-linked (GlcNAc. . .) (Pot N-linked (GlcNAc. . .) (Pot E -> K (in MPS VII).
W; 2AE30884B70D4232 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 898;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cause of mucopolysaccharidosis disease reported in humans, mice
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                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
.6e-50;
                                                                                                                                                                                                                                                                                                                                                                                                    212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Lysosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  degradation
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BGLR_RAT

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AC P06760;

DT 01-JAN-1988 (Rel. 0
DT 01-JAN-1988 (Rel. 0
DT 01-JAN-1988 (Rel. 0
DT 01-JAN-1988 (Rel. 0
DT 25-OCT-2004 (Rel. 4
DE Beta-glucuronidase
GN Name=Gusb; Synonyms
OS Rattus norvegicus (
OC Eukaryota; Metazo;
OC Mammalia; Eutheria;
OX NCBI_TaxID=10116;
RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Preputial gl
RX MEDLINE=87016933; P
RA Adesnik M., Andy R.
RT "Nucleotide sequenc
RT and in vitro insert
RT membranes.";
RL Proc. Natl. Acad. S
RN [2]
RP SEQUENCE OF 14-648
RC TISSUE=Liver;
RX MEDLINE=88183378; P
RA Powell P.P. Kyle J
RT "RAT liver beta-glu
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CC -!- SUBUNIT: Homote
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                                                                                                                                                                                                                        MEDLINE=88183378; PubMed=3355537;
Powell P.P., Kyle J.W., Miller R.D., P
"Rat liver beta-glucuronidase. cDNA cl
expression of a chimeric protein in CO
Biochem. J. 250:547-555(1988).
-!- FUNCTION: Plays an important role
and keratan sulfates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequence of rat and in vitro insertion of it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Preputial gland;
MEDLINE=87016933; PubMed=3463967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-glucuronidase precursor
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 14-648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Gusb; Synonyms=Gus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adesnik M., Andy R.;
                                                             PTM: Undergoes a post-transcriptional proteolytic cleavage n its C-terminal end, which reduces its size by approximately The site of this cleavage has as yet not been determined. SIMILARITY: Belongs to the glycosyl hydrolase 2 family.
                                                                                                                                                  SUBCELLULAR LOCATION: Lysosomal.
                                                                                                                                                                                                         CATALYTIC ACTIVITY: A beta-D-glucuronoside + H(2)0 =
    SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation surropean Bioinformatics Institute. There are no restrictions on its
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45, Last annotation updat
e precursor (EC 3.2.1.31).
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Sciurognathi; Muridae;
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Query Match
Best Local S
Matches 225
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InterPro; IPR006101; Glyco_hydro_21g.
InterPro; IPR006102; Glyco_hydro_21g.
InterPro; IPR006104; Glyco_hydro_2SB.
InterPro; IPR006103; Glyco_hydro_2TIM.
Pfam; PF00703; Glyco_hydro_2; 1.
Pfam; PF02836; Glyco_hydro_2 C; 1.
Pfam; PF02837; Glyco_hydro_2 C; 1.
Pfam; PF02837; Glyco_hydro_2 N; 1.
PROSITE; PR00132; GLHYDRLASE2.
PROSITE; PS00608; GLYCOSYL_HYDROL_F2_1; 1.
Glycoprotein; Glycosidase; Hydrolase; Lyso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; SIGNAL 2: CHAIN 44 CARBOHYD 41-CARBOHYD 59-CARBOHYD 62: CONFLICT 2-CONFLICT 2-CONFLICT 48-SEQUENCE 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M13962; AAA41228.1; -.
EMBL; Y00717; CAA68705.1; -.
PIR; A25047; A25047.
HSSP; P08236; 1BHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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                                                                                                                                                  FRTSHYPYSEEWLDLADRLGILVIDEAPHVGIT------
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TRYDADMGAPYVDVICVNSYLSWYHDYGHLEVIQLQLTSQFENWYKMYQKPIIQSEYGAD
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Pred. No. 2.7e-50;
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InterPro; IPR006101; Glyco_hydro_2.
InterPro; IPR006102; Glyco_hydro_2Ig.
InterPro; IPR006103; Glyco_hydro_2SB.
InterPro; IPR006103; Glyco_hydro_2TIM.
Pfam; PF00703; Glyco_hydro_2; 1.
Pfam; PF02836; Glyco_hydro_2_C; 1.
Pfam; PF02837; Glyco_hydro_2_N; 1.
Pfam; PF02837; Glyco_hydro_2_N; 1.
PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.
PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.
Disease mutation; Glycoprotein; Glycosidase; Hy
  Signal.
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CARBOHYD
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A., AND VARIANT MPS VII HIS-166.

MEDLINE=98190525; PubMed=9521879; DOI=10.1006/geno.1997.5189;

Ray J., Bouvet A., Desanto C., Fyfe J.C., Xu D., Wolfe J.H.,

Aguirre G.D., Patterson D.F., Haskins M.E., Henthorn P.S.;

"Cloning of the canine beta-glucuronidase cDNA, mutation
identification in canine MPS VII, and retroviral vector-mediated
correction of MPS VII cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF019759; AA
HSSP; P08236; 1BHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 018835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Plays an important role in the deand keratan sulfates (By similarity).
-!- CATALYTIC ACTIVITY: A beta-D-glucuronoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 48:248-253(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Beta-glucuronidase precursor (EC 3.2.1.31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9615;
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Name=GUSB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D-glucuronate.
SUBUNIT: Homotetramer (By similarity).
SUBCELLULAR LOCATION: Lysosomal.
DISEASE: Defects in GUSB are the cause
type VII (MPS VII), an inherited diseas
cats, and dogs.
SIMILARITY: Belongs to the glycosyl hyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CANFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Belongs to the
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450
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By similarity.
Beta-glucuronidase.
Proton donor (By similarity).
N-linked (GlcNAc. . .) (Potenti
N-linked (GlcNAc. . .) (Potenti
N-linked (GlcNAc. . .) (Potenti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; ; Fissipedia; Canidae;
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Length CRC64;

Indels

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De Greve H., Nguyen V., Deboeck F. Hernalsteens J.P.;
"T-DNA tagging of the translation Arabidopsis thaliana.";
Plant Sci. 161:685-693 (2001).
                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                               SEQUENCE FROM STRAIN-C24;
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Matches 206; Conserv
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R GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR008979; Gal_bind_like.

InterPro; IPR006101; Glyco_hydro_2:
InterPro; IPR006102; Glyco_hydro_2IG.
InterPro; IPR006103; Glyco_hydro_2SB.
InterPro; IPR006103; Glyco_hydro_2TIM.
Pfam; PF00703; Glyco_hydro_2; 1.
Pfam; PF02836; Glyco_hydro_2; 1.
Pfam; PF02837; Glyco_hydro_2 C; 1.
Pfam; PF02837; Glyco_hydro_2 N; 1.
Pfam; PF02837; Glyco_hydro_2 N; 1.
PROSITE; PR00132; GLHTDRLASE2.
PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.
PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.
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REQUENCE 603 AA; 68433 MW; 7562FE2EB21118DA CRC64
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99.9% imilarity 100.0 ; Conservative  MVRPQRNKKRFILILNG                   XLSQKHIRLYFAAVNTE                  XLSQKHIRLYFAAVNTE                    KVGGFPSKVPDSGTHTV KVGGFPSKVPDSGTHTV	ESULT 1  S-09-270-957-6  Sequence 6, Application US/09270 Patent No. 6641996 GENERAL INFORMATION: APPLICANT: Richard A. Jefferson TITLE OF INVENTION: MICROBIAL - TITLE OF INVENTION: PRODUCTS, A FILE REFERENCE: 190106.405C1 CURRENT APPLICATION NUMBER: US/ CURRENT FILING DATE: 1999-03-17 NUMBER OF SEQ ID NOS: 112 SOFTWARE: FastSEQ for Windows V SEQ ID NO 6 LENGTH: 563 TYPE: PRT ORGANISM: Thermotoga maritima FEATURE: NAME/KEY: VARIANT LOCATION: (1)(563) OTHER INFORMATION: Xaa = Any A S-09-270-957-6	22 22 22 22 22 22 22 22 22 22 23 23 24 25 25 25 25 25 25 25 25 25 25 25 25 25
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Sequence 21, Application US/09270957

Patent No. 6641996

GENERAL INFORMATION:

APPLICANT: Richard A. Jefferson and Jorge E. Mayer

TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GEI

TITLE OF INVENTION: PRODUCTS, AND USES THEREOF

FILE REFERENCE: 190106.405C1

CURRENT APPLICATION NUMBER: US/09/270,957

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 112

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 21

LENGTH: 563

TYPE: PRT
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; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(563)
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                   NIRRMIDRHKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVSMMDAP
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GENERAL INFORMATION:

APPLICANT: Jefferson, Richard A.

APPLICANT: Kilian, Andrzej

APPLICANT: Kilian, Andrzej

APPLICANT: Keese, Paul Konrad

TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 190106.405

CURRENT APPLICATION NUMBER: US/09/149,727

CURRENT FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: US 60/058,263

EARLIER APPLICATION NUMBER: US 60/058,263

EARLIER FILING DATE: 1997-09-09

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin Ver. 2.0

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                                 DKNHPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVTIVLFVMATPE--TDK
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RESULT 4
US-09-270-957-2
; Sequence 2, Application US/09270957
; Patent No. 6641996
; GENERAL INFORMATION:
; APPLICANT: Richard A. Jefferson and Jorge E. Mayer TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GENETITLE OF INVENTION: PRODUCTS, AND USES THEREOF; FILE REFERENCE: 190106.405C1
; CURRENT APPLICATION NUMBER: US/09/270,957
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Bacillus sp.
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Richard A. Jefferson and Jorge E. Mayer

TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES

TITLE OF INVENTION: PRODUCTS, AND USES THEREOF

FILE REFERENCE: 190106.405C1

CURRENT APPLICATION NUMBER: US/09/270,957

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 112

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 602

TYPE: PRT

ORGANISM: Bacillus sp.

US-09-270-957-8
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                                                    GFHDIDPVMFTEEYQVEYYQANHVVFDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVF
                                                                              GIHYDPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVF
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Sequence 15, Application US/09270957

Patent No. 6641996

GENERAL INFORMATION:
APPLICANT: Richard A. Jefferson and Jorge E. Mayer
TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GENETITLE OF INVENTION: PRODUCTS, AND USES THEREOF
FILE REFERENCE: 190106.405C1
CURRENT APPLICATION NUMBER: US/09/270,957
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 602
TYPE: PRT
CORGANISM: Bacillus sp.
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TRDRKPKLAAHVFRERWINI
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RESULT 7 US-09-149-727-4

Sequence 4, Application US/09149727

RESULT 8
US-09-149-727-8
; Sequence 8, Application
; Patent No. 6391547

US/09149727

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APPLICANT: Kilian, Andrzej
APPLICANT: Kilian, Andrzej
APPLICANT: Keese, Paul Konrad
TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 190106.405
CURRENT APPLICATION NUMBER: US/09/149,727
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: US 60/058,263
EARLIER APPLICATION NUMBER: US 60/058,263
EARLIER FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH. 618
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Best Local Similarity 35.6%; Pred. No. 2.6e-73;
Matches 221; Conservative 93; Mismatches 224; Indels
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GENERAL INFORMATION:
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GENERAL INFORMATION:

APPLICANT: Jefferson, Richard A.

APPLICANT: Kilian, Andrzej

APPLICANT: Keese, Paul Konrad

TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GEN

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 190106.405

CURRENT APPLICATION NUMBER: US/09/149,727

CURRENT FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: US 60/058,263

EARLIER APPLICATION NUMBER: US 60/058,263

EARLIER FILING DATE: 1997-09-09

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 607

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Best Local Similarity
Matches 220; Conserv
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ORGANISM: Bacillus
3-09-149-727-8
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RKPKLAAHVFRERWINI
                                ROPKLVAHVLRRLWSEV
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RESULT 9
US-09-270-957-18
; Sequence 18, Application US/09270957
; Patent No. 6641996
; GENERAL INFORMATION:

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; APPLICANT: Richard A. Jefferson and Jorge E. Mayer; TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, G: TITLE OF INVENTION: PRODUCTS, AND USES THEREOF FILE REFERENCE: 190106.405C1
; CURRENT APPLICATION NUMBER: US/09/270,957
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Bacillus sp.
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US-09-270-957-28
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              Sequence 28, Application US/09270957
Patent No. 6641996
GENERAL INFORMATION:
APPLICANT: Richard A. Jefferson and Jorge E. Maritle OF INVENTION: MICROBIAL -GLUCURONIDASE GITITLE OF INVENTION: PRODUCTS, AND USES THEREOFFILE REFERENCE: 190106.405C1
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Best Local Similarity
CURRENT APPLICATION NUMBER: US/09/270,957
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Pred. No. 5.7e-73;
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RESULT 11
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NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 28
LENGTH: 615
TYPE: PRT
ORGANISM: Bacillus sp.
                                                                                                                                                                    Sequence 2, Application US/09862660 Patent No. 6664097 GENERAL INFORMATION:
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Best Local Similarity
Matches 220; Conser
         APPLICANT: Russell, William
APPLICANT: Klaenhammer, Todd
TITLE OF INVENTION: LACTOBACILLUS BETA-GLUCURONIDASE AND DNA ENCODING THE
FILE REFERENCE: 5051.514
CURRENT APPLICATION NUMBER: US/09/862,660
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/206,372
PRIOR FILING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 14
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PatentIn version 3.0
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GENERAL INFORMATION:
APPLICANT: Podsakoff, Gregory
APPLICANT: Watson, Gordon
APPLICANT: Watson, Gordon
APPLICANT: Couto, Linda B.
APPLICANT: Yang, Bin
TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIR
TITLE OF INVENTION: TREATMENT OF LYSOSOMAL DISORDERS
FILE REFERENCE: 0800-0021
CURRENT APPLICATION NUMBER: US/09/715,858
CURRENT FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 16
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; LENGTH: 598
; TYPE: PRT
; ORGANISM: Lactobacillus gasseri
US-09-862-660-2
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US-09-715-858-4
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SOFTWARE: Pa
SEQ ID NO 4
LENGTH: 648
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                               PatentIn Ver. 2.0
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milarity 34.1%;
Conservative 110
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Pred. No. 1.7e-72;
LO; Mismatches 227;
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RESULT 13
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                                                                                                                                                                                                                                                                                     Sequence 12, Application US/09118276 Patent No. 6693185
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Best Local Similarity
Matches 224; Conserv
                                                                                                                                               GENERAL INFORMATION:

APPLICANT: BABIYCHUK, ELENA;

APPLICANT: KUSHNIR, SERGEI;

APPLICANT: DE BLOCK, MARC;

APPLICANT: INZE, DIRK

TITLE OF INVENTION: METHODS AND MEANS TO MODULATE PROGRAMMED

TITLE OF INVENTION: CELL DEATH IN EUKARYOTIC CELLS
                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIXBEY, F
COMPUTER READABLE FORM:
        STREET: 8180 GREENSBORO DRIVE, SUITE CITY: MCLEAN, STATE: VIRGINIA COUNTRY: USA ZIP: 22102
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||||||||||||| | | | | | | 361
NSFRTSHYPYSEEVLQLCDRYGIVVIDECPGVGIVLPQSFGNESLRHHL----EVMEEL 429
                                                                                                                                                                                                                                                                                                                                                                                                NKKGIFTROROPKTSAFILRERYW 623
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; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
US-09-118-276-12
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1010 RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: SCHULMAN, ROBERT M.; SALEN, KENNETH
REGISTRATION NUMBER: 31,196; 43,077
REFERENCE/DOCKET NUMBER: 6201-0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 790-9110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 17-JUL-1998
PRIOR APPLICATION DATA: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM-COMPATIBLE OPERATING SYSTEM: MS-DOS SOFTWARE: ASCII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468 RNYAGNVWYQREVFIPKGWAGQRIVLRFDAVTHYGKVWVNNQEVMEHQGGYTPFEADVTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 EE--GPFTYKTTFYVPKXLSQKHIRLYFAAVNTDCEVFLNGEKVGENHIEYLPFEVDVTG 103
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LOKRWI
                                                                                                                                                               WSIANEPDTRPQGAREYFAPLAEATRKLDPTRPITCVNVMFCDAHTDTISDL----FDVL
                                                                                                                                                                                                                                        WSVANEPESNHPDAEGFFKALYETANEMDRTRPVVMVSMM--DAPDERTRDVALKYFDIV 435
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                                                                                                   EYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRDRQPKLVAHV 555
                                                                                                                                                                                                                                                                                   VIDETAAVGFNLSLGIGFEAGNKPKELYSEEAVNGETQQAHLQAIKELIARDKNHPSVVM
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                                                                    EYQCAWLDMYHRVFDRVSAVVGEQVWNFADFATSQGILRVGGNKKGIFTRDRKPKSAAFL
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RESULT 14

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APPLICANT: Jefferson, Richard A.

APPLICANT: Kilian, Andrzej

APPLICANT: Keese, Paul Konrad

TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENE PRODUCTS AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 190106.405

CURRENT APPLICATION NUMBER: US/09/149,727

CURRENT FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: US 60/058,263

EARLIER FILING DATE: 1997-09-09

NUMBER OF SEQ ID NO8: 71

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 6

LENGTH: 603

TYPE: PRT

ORGANISM: Escherichia coli

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Best Local Simi
Matches 205;
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LOKRWT 589
                                                                                                                                       CLNRYYGWYVQSGDLETAEKVLEKELLAWQEKLHQPIIITEYGVDTLAGLHSMYTDMWSE
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RESULT 15 US-09-270-957-17

Search completed: September Job time : 32 secs

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2005, 19:14:16

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Sequence 17, Application US/09270957

Patent No. 6641996

GENERAL INFORMATION:

APPLICANT: Richard A. Jefferson and Jorge E. Mayer

TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GE

TITLE OF INVENTION: PRODUCTS, AND USES THEREOF

FILE REFERENCE: 190106.405C1

CURRENT APPLICATION NUMBER: US/09/270,957

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 112

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17

LENGTH: 603
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Post-processing: Minimum Match 10%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

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2999 2999 2999 2011 929 929 929 929 929 929	Score
99.9 99.9 99.9 31.0 31.0 31.0	Query Match Length
563 563 563 602 602 602 602	Length
155 148 148 155	DB
US-10-364-649-6 US-10-364-649-21 US-10-369-493-2995 US-10-757-093-20 US-10-757-093-19 US-10-364-649-2 US-10-364-649-15 US-10-364-649-15 US-10-757-093-23 US-10-757-093-23 US-10-757-093-23	ID
Sequence 6, Appli Sequence 21, Appl Sequence 2995, Ap Sequence 20, Appl Sequence 19, Appli Sequence 2, Appli Sequence 2, Appli Sequence 8, Appli Sequence 15, Appli Sequence 23, Appli Sequence 4, Appli	Description

## ALIGNMENTS

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US-10-364-649-6

; Sequence 6, Application US/1036469
; Sequence 6, Application US/1036469
; Sequence 6, Application US/20030229921A1
; GENERAL INFORMATION: USEO030229921A1
; GENERAL INFORMATION: MICROBIAL B-GLUCUROLIDASE GENES, GENE
; TITLE OF INVENTION: MICROBIAL B-GLUCUROLIDASE GENES,
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; TITLE OF INVENTION: MICROBIAL B-GLUCUROLIDASE GENES
; TITLE OF INVENTION: MICROBIAL B-GLUCUROLIDASE
; TITLE OF INVENTION: MICROBIAL B-G
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PRIOR APPLICATION NUMBER: 10/364,649
PRIOR FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: US 09/270,957
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 563
TYPE: PRT
ORGANISM: Thermotoga maritima
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(563)
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-364-649-21
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US-10-364-649-21
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Best Local S
Matches 563
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CURRENT APPLICATION NUMBER: US/10/364,649
CURRENT FILING DATE: 2003-02-12
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                                                               99.9%; Score 2999; DB 15; llarity 100.0%; Pred. No. 1.9e-241; Conservative 0; Mismatches 0;
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APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 2995

LENGTH: 563

TYPE: PRT

ORGANISM: Thermotoga maritima

US-10-369-493-2995
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US-10-369-493-2995
US-10-369-493-2995
; Sequence 2995, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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                                                                                                                                Conservative
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                                                                                                                             Score 2999; DB 15;
Pred. No. 1.9e-241;
D; Mismatches 1;
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RESULT 4
US-10-757-093-20

Sequence 20, Application US/10757093

Publication No. US20050153448A1

GENERAL INFORMATION:
APPLICANT: CAMBIA
ITITLE OF INVENTION: Fungal beta-glucuronidase genes and
FILE REFERENCE: 415

CURRENT APPLICATION NUMBER: US/10/757,093

CURRENT FILING DATE: 2004-01-14

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin version 3.2

SEQ ID NO 20
LENGTH: 563

TYPE: PRT
ORGANISM: Thermotoga maritima

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Best Local Similarity
Matches 562; Conserv
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Pred. No. 1.9e-241;
0; Mismatches 1;
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Publication No. US20050153448A1;
GENERAL INFORMATION:
APPLICANT: CAMBIA
TITLE OF INVENTION: Fungal beta-glucuronidas;
FILE REFERENCE: 415;
CURRENT APPLICATION NUMBER: US/10/757,093;
CURRENT FILING DATE: 2004-01-14;
NUMBER OF SEQ ID NOS: 37;
SOFTWARE: PatentIn version 3.2;
SEQ ID NO 19;
LENGTH: 570;
TYPE: PRT
ORGANISM: Sulfolobus solfataricus
US-10-757-093-19
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Best Local Similarity 39.2%;
Matches 230; Conservative 93
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                                            GITRYHYNPETQKI-----AEDNIRRMIDRHKNHPSVIMWSVANEPESNHPDAEGF
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Pred. No. 2.2e-75;
2; Mismatches 191;
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CURRENT APPLICATION NUMBER: US/10/120,145

CURRENT FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/149,727

PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,263

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/058,263

PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-09

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 602

TYPE: PRT
ORGANISM: Bacillus sp.

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Publication No. US20030157684A1
GENERAL INFORMATION:
APPLICANT: Jefferson, Richard A.
APPLICANT: Kilian, Andrzej
APPLICANT: Keese, Paul Konrad
TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE OF INVENTION: USES THEREOF
FILE REFERENCE: 190106.405
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Best Local Similarity
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                           HKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDV
                                                                      LADREGLVVIDETPAVGV---HLNFMATTGLGEGSERVSTWEKIRTFEHHODVLRELVSR
                                                                                                                                               KFLINNKPFYFKGFGKHEDTPINGRGFNEASNVMDFNILKWIGANSFRTAHYPYSEELMR
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                                                                                                                                                                                                                                                        KKIRTSNRFVEGEFILENARFWSLEDPYLYPLKVELEKDEYTLDI-----GIRTISWDEK 267
                                                                                                                                                                                                                                                                                               GLHRPVKIYTTPFTYVEDISVVTDFNGP---TGTVTYTVDFQ----GKAETVKVSVVDEE
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35.6%; Pred. No. 1.7e-68;
93; Mismatches 224;
                                                                                                            ---PETQKIA----EDNIRRMIDR
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; ORGANISM: Bacillus
US-10-364-649-2
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US-10-364-649-2
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Best Local S
Matches 221
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GENERAL INFORMATION:

APPLICANT: Richard A. Jefferson and Jorge E. Mayer

TITLE OF INVENTION: MICROBIAL B-GLUCURONIDASE GENES

TITLE OF INVENTION: PRODUCTS, AND USES THEREOF

FILE REFERENCE: 190106.405C1

CURRENT APPLICATION NUMBER: US/10/364,649

CURRENT FILING DATE: 2003-02-12

PRIOR APPLICATION NUMBER: 10/364,649

PRIOR FILING DATE: 2003-02-12
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PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
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                   369 HKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDV 427
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DKNHPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVTIVLFVMATPE--TDK
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APPLICANT: Richard A. Jefferson and Jorge E. Mayer
TITLE OF INVENTION: MICROBIAL B-GLUCURONIDASE GENES, GENE
TITLE OF INVENTION: PRODUCTS, AND USES THEREOF
FILE REFERENCE: 190106.405C1
CURRENT APPLICATION NUMBER: US/10/364,649
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: 10/364,649
PRIOR FILING DATE: 2003-02-12
PRIOR FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: US 09/270,957
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-364-649-8
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Best Local Similarity
Matches 221; Conserv
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                                                                   HKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDV
                                                                                                                                                                                              KFLINNKPFYFKGFGKHEDTPINGRGFNEASNVMDFNILKWIGANSFRTAHYPYSEELMR
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ALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHR----KPIFVTEFGADAIA
                                       DKNHPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVTIVLFVMATPE--TDK
                                                                                                                  LADREGLVVIDETPAVGV----HLNFMATTGLGEGSERVSTWEKIRTFEHHQDVLRELVSR
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                                                                                                                                                                                                                                                                                                                                                   GLHRPVKIYTTPFTYVEDISVVTDFNGP---TGTVTYTVDFQ----GKAETVKVSVVDEE
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Sequence 15, Application US/10364649

Publication No. US20030229921A1

GENERAL INFORMATION:
APPLICANT: Richard A. Jefferson and Jorge E. Mayer
TITLE OF INVENTION: MICROBIAL B-GLUCURONIDASE GENES, GITTLE OF INVENTION: PRODUCTS, AND USES THEREOF
FILE REFERENCE: 190106.405C1
CURRENT APPLICATION NUMBER: US/10/364,649
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: 10/364,649
PRIOR FILING DATE: 2003-02-12
PRIOR FILING DATE: 2003-02-12
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 602
TYPE: PRT
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US-10-364-649-15
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Sequence 23, Application US/10757093;
Publication No. US20050153448A1;
GENERAL INFORMATION:
APPLICANT: CAMBIA
TITLE OF INVENTION: Fungal beta-glucuronidase genes and gene proceedings of the process of the Reference: 415
CURRENT APPLICATION NUMBER: US/10/757,093;
CURRENT FILING DATE: 2004-01-14;
NUMBER OF SEQ ID NOS: 37;
SOFTWARE: PatentIn version 3.2;
SEQ ID NO 23;
LENGTH: 602
TYPE: PRT
ORGANISM: Staphylococcus sp.
US-10-757-093-23
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APPLICANT: Jefferson, Richard A.

APPLICANT: Kilian, Andrzej

APPLICANT: Kilian, Andrzej

APPLICANT: Keese, Paul Konrad

TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, G

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 190106.405

CURRENT APPLICATION NUMBER: US/10/120,145

CURRENT FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/

PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-08

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US

PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-09

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 618
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                      GIHYDPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVF
                                                             VAELIDVIALNRYNGWYFDGGDLEAAKVHLR---QEFHAWNKRCPGKPIMITEYGADTVA
                                                                                                                                                              HKNHPSVIMWSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDV
                                                                                                                                                                                               KFLINNKPFYFKGFGKHEDTPINGRGFNEASNVMDFNILKWIGANSFRTAHYPYSEELMR
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                                                                                                                                                                                                                                                                                                                                                                                                                                GIIRPVLIEFTDHARILDIWVDTSESEPEKKLGKVKVKIEVSEEAVGQEMTIKLG--EEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRDGMNRVTVAVDNIL------DDSTLPVGLYSERHEEGLGKVIRNKPNFDFFNYA
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 GFHDIDÞVMFTEEYQVEYYQANHVVFDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVF
                                                                                    ALKYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHR----KPIFVTEFGADAIA 483
                                                                                                                               DKNHPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVTIVLFVMATPE--TDK
                                                                                                                                                                                                                               LADRIGILVIDEAPHYGITRYHYN-----PETQKIA-----EDNIRRMIDR
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US-10-120-145-8
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US-10-120-145-8
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CURRENT FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/149,727

PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,263

PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-09

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 8

LENGTH: 607
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APPLICANT: Kilian, Andrzej
APPLICANT: Kilian, Andrzej
APPLICANT: Keese, Paul Konrad
TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 190106.405
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YDPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRD
                                                              LIDVIALNRYNGWYFDGGDLEAAKVHLR---QEFHAWNKRCPGKPIMITEYGADTVAGFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GMNRVTVAVDNIL-----DDSTLPVGLYSERHEEGLGKVIRNKPNFDFFNYAGLH 178
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                                                                                               YFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHR----KPIFVTEFGADAIAGIH
                                                                                                                                                                            HPSVIMWSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDVALK 430
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Sequence 18, Application US/10364649

Publication No. US20030229921A1

GENERAL INFORMATION:

APPLICANT: Richard A. Jefferson and Jorge E. Mayer

ITILE OF INVENTION: MICROBIAL B-GLUCURONIDASE GENES, GENES, TITLE OF INVENTION: PRODUCTS, AND USES THEREOF

FILE REFERENCE: 190106.405C1

CURRENT APPLICATION NUMBER: US/10/364,649

CURRENT FILING DATE: 2003-02-12

PRIOR APPLICATION NUMBER: 10/364,649

PRIOR FILING DATE: 2003-02-12

PRIOR FILING DATE: 2003-02-12

PRIOR FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 112

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18
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US-10-364-649-18
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Best Local Similarity
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DIDPVMFTEEYQVEYYQANHVVFDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVFTRD
                                 YDPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRD
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                                                                           LIDVIALNRYNGWYFDGGDLEAAKVHLR----QEFHAWNKRCPGKPIMITEYGADTVAGFH
                                                                                                                                                   HPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVTIVLFVMATPE--TDKVAE
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Sequence 28, Application US/10364649
; Publication No. US20030229921A1
; GENERAL INFORMATION:
; APPLICANT: Richard A. Jefferson and Jorge E. Mayer
TITLE OF INVENTION: MICROBIAL B-GLUCURONIDASE GENES, G
TITLE OF INVENTION: PRODUCTS, AND USES THEREOF
; FILE REFERENCE: 190106.405C1
; CURRENT APPLICATION NUMBER: US/10/364,649
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 10/364,649
; PRIOR FILING DATE: 2003-02-12
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Bacillus sp.
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DIDPVMFTEEYQVEYYQANHVVFDEFENFVGEQAWNFADFATSQGVMRVQGNKKGVFTRD
                                                                                                     YFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHR----KPIFVTEFGADAIAGIH
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                                                                                                                                                                                HPSVIMWSVANEPESNHPDAEGFFKALYETANEMD-RTRPVVMVSMMDAPDERTRDVALK
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                                YDPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQNVRRPILNHKGVFTRD
                                                                                                                                              HPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVTIVLFVMATPE--TDKVAE
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; SEQ ID NO 2
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Scopulariopsis sp. isolate RP38.
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Best Local :
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CURRENT FILING DATE: 2004-01-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.2
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nes 219; Conserv
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                             RDROPKLVAHVLRRLW
                                                           HAVDEVLWSEEYQTNLLRMSHKVFDSIDSIVGEHVWNFADFQTPHTGVNRVDGNKKGVFT
                                                                                     HYDPPQMFSEEYQAELVEKTIRLLLKKDYIIGTHVWAFADFKTPQ-NVRRPILNHKGVFT
                                                                                                                                               AL--KYFDIVCVNRYYGWYIYQGRIEEGLQALEKDIEELYARHRKPIFVTEFGADAIAGI
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  chosen parameters:
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AX827491
RATGLCB
AR344265
AX147654
MUSGUSS
                                                            AR428149
AE001766
AF012423
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AF084552
CQ57570
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                                        AR428149 Sequence
AE001766 Thermotog
AF012423 Felis cat
AF012424 Felis cat
AF019759 Canis fam
AF084552 Chloroceb
CQ575703 Sequence
BC014142 Homo sapi
BT010073 Drosophil
AR344264 Sequence
AX147652 Sequence
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6.7	6.7	6.8	6.8	7.2		7.6	7.7	8.2	8.2	8.2	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	9.2	9.3	9.3	9.4	9.4	9.4
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AF305918 Escherich	BD185061 Nucleic a	AP005222 Corynebac	AF305917 Escherich	AJ420784 Clostridi	AP003185 Clostridi	AC084452 Caenorhab	AR428153 Sequence	AY069329 Drosophil	BT012475 Drosophil	AE006894 Sulfolobu	BV175016 sqnm76123	AF354046 Binary ve	AF354045 Binary ve	AY452736 Reporter	BD074927 Microbial	AR210802 Sequence	AF354047 Synthetic	Continuation (26 o	CQ363720 Sequence	AJ720880 Gallus ga	J03047 Mouse beta-	M19279 Mouse beta-	BC071226 Mus muscu	M63836 Mouse beta-	M28541 Mouse beta-

## ALIGNMENTS

REFERENCE AUTHORS TITLE KEYWORDS SOURCE ORGANISM LOCUS
DEFINITION
ACCESSION
VERSION RESULT 1 AR428149 뮍 δ S 멍 Ş В 밁 Ś ORIGIN FEATURES Query Match 99.9%; Score 1688; D Best Local Similarity 100.0%; Pred. No. 0; Matches 1689; Conservative 0; Mismatches JOURNAL source 181 121 121 61 61 Sequence AR428149 سر Unclassified.
1 (bases 1 to 1689)
Jefferson, R.A. and Mayer, J.E.
Microbial .beta.-glucuronidase genes, Unknown Unknown. AR428149.1 GI:40187542 AR428149 NAACTTTCACAAAAACACATCAGACTTTACTTTGCTGCGGTGAACACGGACTGCGAGGTC CAGGATCTGTGCTACGAAGAAGGACCCTTCACCTACAAAACCACCTTCTACGTTCCGAAG CAGGATCTGTGCTACGAAGAAGGACCCTTCACCTACAAAACCACCTTCTACGTTCCGAAG CTTGAAGTAACCAGCAAAGACAGACCAATCGCCGTTCCTGGAAGCTGGAATGAGCAGTAC ATGGTAAGACCGCAACGAAACAAGAAGAGATTTATTCTTATCTTGAATGGAGTTTTGGAAT TTCCTCAACGGAGAGAAAGTGGGAGAGAATCACATTGAATACCTTCCCTTCGAAGTAGAT NAACTTTCACAAAAACACATCAGACTTTACTTTGCTGCGGTGAACACGGACTGCGAGGTC ATGGTAAGACCGCAACGAAACAAGAAGAGATTTATTCTTATCTTGAATGGAGTTTGGAAT US 6641996-A 14 04-NOV-2003; 14 from Location/Qualifiers
1. .1689 /organism="unknown" /mol\_type="genomic DNA" patent 1689 bp US 6641996. DB DNA 6 gene products and **,** Length 1689; Indels linear PAT 18-DEC-2003 <u>,</u> Gaps 240 240 180 180 120 120 60

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                                            GACGAGAGAACAAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTAC
                                                              GACGAGAGAACAAGAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTAC
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                                                                                                                                                                                                                                                 AACATAAGAAGAATGATCGACAGACAAGAACCATCCCAGTGTGATCATGTGGAGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTTATCCTCTCAAGGTGGAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGACAGGAGATGACGATCAAACTTGGAGAGGAGAGAAAAAAGATTAGAACATCCAACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGACAGGAGATGACGATCAAACTTTGGAGAGGAAGAAAAAAGATTAGAACATCCAACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAACCGGAGAAGAACTTGGAAAAGTGAAAGTGAAGATAGAAGTCTCAGAAGAAGCGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAACCGGAGAAGAAACTTGGAAAAGTGAAAGTGAAGATAGAAGTCTCAGAAGAAGCGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAAGTTTTCCACCTGCAAACTTCGACTTCTTCCCCCTACGGTGGAATCATAAGGCCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAAGTTTTCCACCTGCAAACTTCGACTTCTTCCCCTACGGTGGAATCATAAGGCCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAGTGGGAGGATTTCCCTCGAAGGTTCCAGACAGCGGCACTCACACCGTGGGATTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGACGGGAAAGTGAAATCCGGAGAGAACGAACTCAGGGTGGTTGTTGAGAACAGATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGACGGGGAAAGTGAAATCCGGAGAGAACGAACTCAGGGTGGTTGTTGAGAACAGATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCCTCAACGGAGAAAGTGGGAGAGAATCACATTGAATACCTTCCCTTCGAAGTAGAT
                                                                                                                                                                                                                               AACATAAGAAGAATGATCGACAGACACAAGAACCATCCCAGTGTGATCATGTGGAGTGTG
                                                                                                                                                                                                                                                                                                                                                    TACAGTGAAGAGTGGCTGGATCTTGCCGACAGACTCGGAATCCTTGTGATAGACGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGATCAGCTGGGACGAGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMAGTGGGAGGATTTCCCTCGAAGGTTCCAGACAGCGGCACTCACACCGTGGGATTTTTT
                                                                                                         ACTGCCAATGAAATGGATCGAACACGCCCCGTTGTCATGGTGAGCATGATGGACGCACCA
                                                                         1320
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gene CDS	REFERENCE AUTHORS  TITLE JOURNAL FEATURES SOURCE	ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED	Qy 16 Db 16 RESULT 2 AEOO1766/C LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE	Qy 15 Db 15 Qy 16 Db 16	Db 13 Oy 13 Oy 14 Db 14 Db 15 Oy 15
/organism="Thermotoga maritima MSB8" /mol_type="genomic DNA" /strain="MSB8" /db_xref="taxon:243274" 811607 /locus_tag="TM1058" 811607 /locus_tag="TM1058" /note="similar to GB:AE000666 percent identity: 48.70; identified by sequence similarity; putative" /codon_start=1	2 (bases 1 to 12583) 2 (bases 1 to 12583) Nelson,K.E., Clayton,R.A., Gill,S.R., Gwinn,M.L., Dodson,R.J., Haft,D.H., Hickey,E.K., Peterson,J.D., Nelson,W.C., Ketchum,K.A., McDonald,L., Utterback,T.R., Malek,J.A., Linher,K.D., Garrett,M.M., Stewart,A.M., Cotton,M.D., Pratt,M.S., Phillips,C.A., Richardson,D., Heidelberg,J., Sutton,G.G., Fleischmann,R.D., White,O., Salzberg,S.L., Smith,H.O., Venter,J.C. and Fraser,C.M. Direct Submission Submitted (01-JUN-1999) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers 1. 12583	Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotogae.  1 (bases 1 to 12583)  Nelson,K.E., Clayton,R.A., Gill,S.R., Gwinn,M.L., Dodson,R.J., Haft,D.H., Hickey,E.K., Peterson,J.D., Nelson,W.C., Ketchum,K.A., McDonald,L., Utterback,T.R., Malek,J.A., Linher,K.D., Garrett,M.M., Stewart,A.M., Cotton,M.D., Pratt,M.S., Phillips,C.A., Richardson,D., Heidelberg,J., Sutton,G.G., Fleischmann,R.D., Eisen,J.A., White,O., Salzberg,S.L., Smith,H.O., Venter,J.C. and Fraser,C.M. Evidence for lateral gene transfer between Archaea and bacteria from genome sequence of Thermotoga maritima  L Nature 399 (6734), 323-329 (1999)  10360571	81 AGTGAGGTT 1689  81 AGTGAGGTT 1689  81 AGTGAGGTT 1689  81 AGTGAGGTT 1689  AE001766  Thermotoga maritima MSB8 section 78 of 136 of the complete genome. AE001766.1 GI:4981600  Thermotoga maritima MSB8	61 TGGGCCTTTGCAGATTTTAAGACTCCTCAGAATGTGAGAAGACCCATTCTCAACCACAAG 1620	21 TACGGCTGGTACATCTATCAGGGAAGGATAGAAGAAGACTTCAAGCTTCTGGAAAAAGAC 1380 81 ATAGAAGAGCTCTATGCAAGGCACAGAAAGCCCCATCTTTGTCACAGAATTCGGTGCGAAC 1440 81 ATAGAAGAGCTCTATGCAAGGCACAGAAAGCCCCATCTTTGTCACAGAATTCGGTGCGGAC 1440 81 ATAGAAGAGCTCTATGCAAGGCACCAGAAAGCCCATCTTTGTCACAGAATTCCGGTGCGGAC 1440 81 ATAGAAGAGCTCTATGCAAGGCACCAGAAAAGTTCTCTCCGAAGAGTACCAAGCAGAG 1500 81 GCGATAGCTGGCATCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAG 1500 81 GCGATAGCTGGCATCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAG 1500 81 ATAGAAGAGCTGCTCCATCTACGATCCACCTCAAATGTTCTCCCGAAGAGTACCAAGCAGAG 1500 81 ATAGAAGAGCTGCTCATCTACGAAAAAAAAAGACTACATCGGAACACACAC

gene

CDS

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GFGTLFLIAGSLGALNGYFLKIQYEPPYKPREASVSITKAVKFLLKEEHFKNFLFGFA
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complement(1962. 3272)
                                                                                                                                                                                                                                                 MTIDVLRIISEEKTEWKELYVKVLRRAQRYAVVLERMISPEGTFPIIGRSITYRTAVFHLLSQLSLLHLLPASLSPAQVRCALTAVLRRIFENPSTFDENGWLKIGVIGSQPSLGEEYITTGSLYLCTTVFLPLGLPTSDPFWRDPCKKWTNKKVWEGEDVAPDRALED"
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LLFSAMIETFFFFAGEEWDSTKVDLILKNVESWYKGDGAYGDGPFFRWDYYNSFVIYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (3382..4545)
/locus_tag="TM1061"
complement (3382..4545)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FWNFAIGVGTVYINVMLLKEVEFSYLQISVLNAVGMFIGTLFQPFWGKLGDRYGFQYFLKVCLWIHAIVILLWTLTPRSFLYVFFLQIIIGIFVTAGTSQLVFYTLMYTAPSSLKTEAFSVFNSLSNLSLFAGSLVASVLVASLENISLPFGISAIRLTMFISFFLRASAAYIISRMDLGTPQKVDSLIQAVKESFFSGTVPWIRERLNTLNIFRRKR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (1650. .1913)
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identity: 48.70; identified
                                 identity: 57.73; putative"
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/note="similar to PID:642973 PID:14446 PID:412358 percent
identity: 57.73; identified by sequence similarity;
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codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tag="TM1060"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .3272)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein"
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SgS

gene

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complement (6284. 7309)
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/note="similar to SP:P42065 P
identity: 75.31; identified by
putative"
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GDVPDPRNMPKGCRFHPRCPYMKGICDEREPVEVEVGPEHRVSCFLYGGEKDGAS"
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SHDLGVVEHITNRVAVMYVGRIVELAETEELFSSPKHPYTEALLSAVPKPDPKRKRKK
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/note="similar to GB:AE000657 percent identity:
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complement (6284. .7309)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="myrpornkkrfililingvwnlevtskdrpiavpgswneoyodlc yeegpftykttfyvpkelsokhirlyfaavntdcevflngekvgenhieylpfevdvt gkvksgenelrvvvenrlkvggfpskvpdsgthtvgffgsfpaanfdffpyggiirpv lieftdharildiwvdtsesepekklgkvkvkievseeavgoemtiklgeeekkirts nrfvegefilenarfwsledpylyplkvelekdeytldigirtiswdekrlylngkpv flkgfgkheefpvlgogtfyplmikdfnllkwinansfrtshypyseewldladrlgilvideaphvgitryhynpetokiaednirmidrhknhpsvimwsvanepesnhpdae
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                                             complement (9420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus_tag="TM1064"
complement/page"
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/locus_tag="TM1066"
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transl_table=11/
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/transl_table=11
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/db_xref="GI:4981609"
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/locus_tag="TM1066"
/note="similar to SP:P42062 P:
identity: 62:93; identified b)
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/codon_start=1
/transI_table=11
/product="oligopeptide ABC transtage"
/brotein_id="AAD36141.1"
/db_xref="GI:4981607"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; 1 (bases 1 to 2153)

Fyfe, J.C., Kurzhals, R.L., Lassaline, M.E., Henthorn, F Wang, P., Wolfe, J.H., Giger, U., Haskins, M.E., Patters
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                                                            Felis catus (cat)
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/mol_type="mRNA"
/db_xref="taxon:9685"
/tissue_type="liver"
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GQLQVPNAHLWWPYLMHEHPAYLYSLEVRLTAQTAAGSVSDFYTLPVGIRTVAVTEHQ
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QLCDRYGIVVIDESPGVGIVLVESYSNVSLQHHLEVMEELVRRDKNHPAVVMWSVANE
PASFLKPAGYYFKTLIAHTKALDPSRPVTFVTNSNYEADLGAPYVDVICVNSYYSWYH
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/note="lysosomal hydrolase; lysosomal exooligosaccharidase /note="lysosomal hydrolase; lysosomal exooligosaccharidase in stepwise degradation of glucuronic acid-containing oligosaccharide sidechains of proteoglycans"
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Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fe.
1 (bases 1 to 2014)
3 Fyfe, J.C., Kurzhals, R.L., Lassaline, M.E., Henthorn, P.S.
Wang, P., Wolfe, J.H., Giger, U., Haskins, M.E., Patterson,
Sun, H., Jain, S. and Yuhki, N.
Molecular basis of feline beta-glucuronidase deficiency
model of mucopolysaccharidosis VII
Genomics 58 (2), 121-128 (1999)
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                                                                                                            CCGTATGTGGACGTCATCTGTGAATAGTTACTACTCTTGGTATCATGACTATGGTCAC
                                                                                                                                       AAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACATCTATCAGGGAAGG
                                                                                                                                                                                                                                  CGCTATGGGATCGTGGTCATCGACGAGAGTCCCCGGTGTGGGCCATCGTGCTGGTCGAGAGC
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                                               ATGGAGGTGATTCAGCTGCAGCTGGCAACCCAGTTTGAGAACTGGTATAGGACCTATCAG
                                                                            ATAGAAGAAGGACTTCAAGCTCTGGAAAAAGACATAGAAGAGCTCTATGCAAGGCACAGA
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YWKLANETRYPWSAVKSQCLENSPFTL"
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2. .1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="mutant beta-glucuronidase"
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/db_xref="GI:4102553"
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/allele="MPS
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3.2.1.31"
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Pred. No. 2e-40;
0; Mismatches 416;
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                                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
                                                                                                                                                                                                                                                               note="lysosomal
                                                                                                                                                                                                                                                                              /gene="GUSB"
/EC_number="
                                                                                                                                                                                                                                                                                                                          gene="GUSB"
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'db_xref="taxon:9615"
L._.2199
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 2199)

Ray, J., Bouvet, A., DeSanto, C., Fyfe, J.C., Xu, D., Wolfe, J.H., Aguirre, G.D., Patterson, D.F., Haskins, M.E. and Henthorn, P.S. Cloning of the canine beta-glucuronidase cDNA, mutation identification in canine MPS VII, and retroviral vector-mediated correction of MPS VII cells Genomics 48 (2), 248-253 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pennsylvania School of Veterinary Medicine, Philadelphia, PA 19104, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATCAAAAACGCAAAGAATACGTGGTCGGAGAGCTCATCTGGAACTTTGCCGATTTTATG
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                                                                                                                                                                                         GACTCCTCAGAATGTGAGAAGACCCATTCTCAACCACAAGGGTGTTTTCACAAGAGACAG
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Best Local Similarity
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Human Genetics Unit, Crewe Road,
Location/Qualifiers
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1 (bases 1 to 2155)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Partial cDNA sequence
TGGATCTTGCCGACAGACTCGGAATCCTTGTGATAGACGAAGCCCCCGCACGTTGGTATCA 1036
                                                                                                                                                                                                             AGAAGAGGCTCTATCTGAACGGGAAAACCTGTCTTTTTGAAGGGCCTTTGGAAAGCACGAGG
                                                     TTCGCTGGCTTGGTGCCAATGCCTTCCGCACCACCACTACCCCTACGCCGAGGAAGTGC
                                                                                      TGAAGTGGATCAACGCGAATTCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGC
                                                                                                                     ATGCGGACATCCGAGGGAAGGGCTTCGACTGGCCGCTGCTGGAAGGACTTCAACCTGC
                                                                                                                                                      AATTCCCCGTTCTGGGGCAGGGCACCTTTATCCATTGATGATAAAAGACTTCAACCTTC
                                                                                                                                                                                         AAAGCCAGTTCCTCATCAATGGGAAACCTTTCTATTTCCACGGTGTCAACAAGCATGAGG
                                                                                                                                                                                                                                                            TGGGGCCTGTGTCTGACTTCTACACCCTCCCTGTGGGGATCCGCACTGTGGCTGTCACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to Homo sapiens beta-glucuronidase; beta-D-glucuronoside; glucuronosohydrolase; glucuronohydrolase"
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/EC_number="3.2.1.31"
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/protein_id="AAC34593.1"
/db_xref="GI:3549609"
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/mol_type="mRNA"
/db_xref="taxon:9534"
/cell_line="COS7"
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Pred. No. 1.5e-35;
D; Mismatches 436;
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CQ575703
                                                                                                                                                                                                                             Drosophila sp.
Drosophila sp.
Drosophila sp.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                              Venter, J.C., Adams, M., Li, P.W. and Myers, E.W.

Detection kits, such as nucleic acid arrays, for detecting the expression of 10,000 or more Drosophila genes and uses thereof Patent: WO 0171042-A 3461 27-SEP-2001;

PE Corporation (NY) (US)
Location/Qualifiers
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/mol_type="unassigned
/db_xref="taxon:7242"
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                 2182 bp
ase, beta,
                  mRNA linear PRI 29-JUN-2004 mRNA (cDNA clone MGC:20659
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REFERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Gay, L.J., Hulyk, S.W.,
Villalon, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
L Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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BC014142.2
MGC.
                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLNL at: http://image.lln Series: IRAL Plate: 30 Row: o Column: 15
This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (10-SEP-2001) National Institutes of Health, Mammalian Submitted (10-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
On Dec 19, 2003 this sequence version replacement: MGC help desk
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1 (bases 1 to 2182)
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/clone="MGC:20659 IMAGE:4662011"
/tissue type="Colon, adenocarcing
/clone_lib="NIH_MGC_15"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                  CAGACAAGGGGGCTCCGTATGTGGATGTGATCTGTTTGAACAGCTACTACTCTTGGTATC
                                                                                                                                       GAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACA 1333
                                                                                                                                                                                              TGGACCCCTCCCGGCCTGTGACCTTTGTGAGCAACTCTAACTATGCAG-------
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         /db_x1
2...1957
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RYWKIANETRYPHSVAKSQCLENSLFT"
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                                                                                                                                                    xref="MIM:253220"
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Conservative 10.3%; <u>,</u> Score 174; DB 9; I Pred. No. 1.9e-35; 0; Mismatches 430; Length 2182; Indels 21;

TGGAACTTGAAAAAAGACGAGTACACTCTGGACATCGGAATCAGAACGATCAGCTGGGACG TGGATCGAACACGCCCCGTTGTCATGGTGAGCATGATGGACGCACCAGACGAGAGAACAA 1273 CGTCCCACCTAGAATCTGCTGGCTACTACTTGAAGATGGTGATCGCTCACACCAAATCCT AGTCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCCTTTATGAGACTGCCAATGAAA 121: TGGTGCGTAGGGACAAGAACCACCCCGCGGTCGTGATGTGGTCGTGGCCAACGAGCCTG TGCAGATGTGTGACCGCTATGGGATTGTGGTCATCGATGAGTGTCCCGGCGTGGGCCTGG AGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTGAAGGGCTTTGGAAAGCACGAGG TGGGGCCTGTGTCTGACTTCTACACACTCCCTGTGGGGATCCGCACTGTGGCTGTCACCA CGCTGCCGCAGTTCTTCAACAACGTTTCTCTGCATCACCACATGCAGGTGATGGAAGAAG CAAGGTACCA---CTACAATCCCGAGACTCAGAAGATAGCAGAAGACATAAGAAGAA 1093 TGGATCTTGCCGACAGACTCGGAATCCTTGTGATAGACGAAGCCCCGCACGTTGGTATCA 1036 TTCGCTGGCTTGGTGCCAACGCTTTCCGTACCAGCCACTACCCCTATGCAGAGGAAGTGA TGAAGTGGATCAACGCGAATTCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGC AATTCCCCGTTCTGGGGCAGGGCACCTTTTATCCATTGATGATAAAAGACTTCAACCTTC AGAGCCAGTTCCTCATCAATGGGAAACCTTTCTATTTCCACGGTGTCAACAAGCATGAGG 976 1418 1358 1153 1298 1238 1178 916 856 998 796 1118 1058

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REFERENCE
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                                                                                                                                                                       source
                                                                                                                                                                                                                                                                           Hawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2321)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-AUG-2003) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA
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Drosophila melanogaster LD10588
מאסיים
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Sequence submitted by:
Berkeley Drosophila Genome Project
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                                                                                                                                                                                                 cdna@fruitfly.berkeley.edu.
Location/Qualifiers
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ATGCAAGGCACAGAAAGCCCATCTTTGTCACAGAATTCGGTGCGGACGCGATAGCTGGCA 1453
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                                                                                                                                                                                                           GAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACA 1333
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Podsakoff,G. and Watson,G.
Recombinant adeno-associated virus virions
lysosomal disorders
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                 ATGCGGACATCCGAGGGAAGGGCTTCGACTGGCCGCTGCTGGTGAAGGACTTCAACCTGC
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 TGGTGCGTAGGGACAAGAACCACCCCGCGGTCGTGATGTGGTCTGTGGCCAACGAGCCTG
                                                                             CAAGGTACCA---CTACAATCCCGAGACTCAGAAGATAGCAGAAGACAACATAAGAAGAA
                                                                                                                           TGGATCTTGCCGACAGACTCGGAATCCTTGTGATAGACGAAGCCCCCGCACGTTGGTATCA 1036
                                                                                                                                                        TTCGCTGGCTTGGTGCCAACGCTTTCCGTACCAGCCACTACCCCTATGCAGAGGAAGTGA 1177
                                                                                                                                                                               TGAAGTGGATCAACGCGAATTCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGC
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                                                    CGCTGCCGCAGTTCTTCAACAACGTTTCTCTGCATCACCACATGCAGGTGATGGAAGAAG
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    ТGAAAAGACGAŢĊAGGCTCCTTTTGAAAAAAGACŢACAŢĊĀŢĊĢĢAACAĊĀŢĠŢĠĢĠ

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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unknown"
/mol_type="genomic
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AX147652
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                                                                                                                                                                                                                                                                                                                          Patent: WO O
Avigen, Inc.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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offlingkpfyfhgvnkhedadirgkgfdwpllvkdfnllrwlganafrtshypyaeev
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/db_xref="taxon:9606"
1. ..1956
MQMCDRYGIVVIDECPGVGLALPQFFNNVSLHHHMQVMEEVVRRDKNHPAVVMWSVAN
                                                                                                                                  /note="unnamed protein product"
/codon_start=1
/protein_id="CAC41170.1"
/db_xref="GI:14346709"
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                    GAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACA
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ACGACTACGGGCACCTGGAGTTGATTCAGCTGCAGCTGGCCACCCAGTTTGAGAACTGGT
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="M15182"
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                                                                                                                                                                                                                                                                                 Original source text: Human fibroblasts cDNA clone pHUGF and placenta cDNA clones pHUGP13 and pHUGP15.

Draft entry and copy of computer-readable sequence of [1] kindly provided by R.D.Miller, 08-MAY-1987.

Four potential N-linked glycosylation sites are located at bases 543-551, 840-848, 1284-1292 and 1917-1925. Potential poly-A signals were found 25 and 48 bp upstream of the poly-A site at nucleotides 2139-2144 and 2162-2167 respectively.

Two types of mRNA exit due to alternative splicing. The short form, lacking bases 939-1091 below, encodes a protein lacking beta-glucuronidase activity.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M15182.1 GI:183232
alternative splicing; beta-D-glucuronoside glucuronosohydrolase;
beta-glucuronidase; glucuronidase; glucuronohydrolase; hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oshima, A., Kyle, J.W., Miller, R.D., Hoffmann, J.W., Powell, P.P., Grubb, J.H., Sly, W.S., Tropak, M., Guise, K.S. and Gravel, R.A. Cloning, sequencing, and expression of cDNA for human beta-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2191)
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                                                                                                                        /product="glucuronidase-b
27. .1982
/db_xref="GDB:G00-120-025"
/translation="MARGSAVAWAALGPLLWGCALGLQGGMLYPQESPSRECKELDGL
WSFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVPSSFNDISQDWRLRHFVGWVWYE
                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                           /proteIn_id="AAA52561.1"
/db_xref="GI:183233"
                                                                                                                                                 /gene="GUSB"
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                                                                                       note="beta-glucuronidase"
                                                                                                     gene="GUSB"
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AGTCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCCTTTATGAGACTGCCAATGAAA 1213
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TCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAGCTCGTTGAAAAG- 1512
                                                                                                         ATGCAAGGCACAGAAAGCCCCATCTTTGTCACAGAATTCGGTGCGGACGCGATAGCTGGCA 1453
                                                                                                                                                                                          ACGACTACGGGCACCTGGAGTTGATTCAGCTGCAGCTGGCCACCCAGTTTGAGAACTGGT
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                                                              ATAAGAAGTATCAGAAGCCCATTATTCAGAGCGAGTATGGAGCAGAAACGATTGCAGGGT 1671
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PLPSRLRITIAINNTLTPTTLPPGTIQYLTDTSKYPKGYFVQNTYFDFFNYAGLQRSV
LLYTTPTTYIDDITVTTSVEQDSGLVNYQISVKGSNLFKLEVRLLDAENKVVANGTGT
QGQLKVPGVSLWWPYLMHERPAYLYSLEVQLTAQTSLGPVSDFYTLPVGIRTVAVTKS
QFLINGKPFYFHGVNKHEDADIRGKGFDWPLLVKDFNLLRWLGANAFRTSHYPYAEEV
MQMCDRYGIVVIDECPGVGLALPQFFNNVSLHHHMQVMEEVVRRDKNHPAVVMWSVAN
EPASHLESAGYYLKMVIAHTKSLDPSRPVTFVSNSNYAADKGAPYVDVICLNSYYSWY
HDYGHLELIQLQLATQFENWYKKYQKPIIQSEYGAETIAGFHQDPPLMFTEEYQKSLL
EQYHLGLDQKRRKYVVGELIWNFADFMTEQSPTRVLGNKKGIFTRQRQPKSAAFLLRE
RYWKIANETRYPHSVAKSQCLENSPFT"
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Submitted (07-JAN-1988) Miller R.D., E.A.
Biochemistry, St. Louis University School
Grand Blvd., St. Louis, MO, 63104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Norway rat)
Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat liver beta-glucuronidase. cDNA cloning, and expression of a chimeric protein in COS Biochem. J. 250 (2), 547-555 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Powell, P.P., Kyle, J.W., Miller, R.D., Pantano, J., Grubb, J.H. and Sly, W.S.
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YLMHEHPAYLYSLEVTMTTPESVSDFYTLPVGIRTVAVTKSKFLINGKPFYFQGVNKH
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VGIVLPQSFGNVSLRHHLEVMDELVRRDKHPAVVMWSVANEPVSSLKPAGYYFKTLI
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2391
                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Sprague-Dawley"
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                                   CAACCCAAACTCGTTGCTCATGTACTGAGA 1671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boess, F., Suter-Dick, L. and Wolf, D. Methods for the toxicity prediction of Patent: EP 1344834-A 225 17-SEP-2003; F. HOFFMANN-LA ROCHE AG (CH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                              AGACTCGGAATCCTTGTGATAGACGAAGCCCCCGCACGTTGGTATCACAAGGTACCA---C
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CCTCAAATGTTCTCCGAAGAGTACCAAGCAGAGCTCGTTGAAAAGACGATCAGGCTCCTT 1527
                             AAGCCAATTATCCAGAGCGAGTATGGAGCAGACGCCGTCTCGGGGGCTTCATGAGGATCCA
                                                    AAGCCCATCTTTGTCACAGAATTCGGTGCGGACGCGATAGCTGGCATCCACTACGATCCA 1467
                                                                                     CTGGAGGTGATTCAGCTGCAGCTGACTAGCCAGTTTGAGAACTGGTATAAGATGTACCAG
                                                                                                                ATAGAAGAAGGACTTCAAGCTCTGGAAAAAGACATAGAAGAGCTCTATGCAAGGCACAGA 1407
                                                                                                                                            CCGTACGTGGACGTGATTTGTGTGAACAGTTACTTATCCTGGTATCATGACTACGGGCAT
                                                                                                                                                                        AAGTACTTCGACATCGTCTGTGAACAGGTACTACGGCTGGTACATCTATCAGGGAAGG 1347
                                                                                                                                                                                                   CCTGTGACCTTTGTGAGCAATA-----CCAGATATGACGCAGACATGGGGGCC
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/mol_type="unassigned DNA"
/db_xref="taxon:10116"
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Pred. No. 1.6e-33;
0; Mismatches 432;
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                                                                                                                                                  AACCCCAAGATGGCAGCCTTCATTTTGCGA
                                                                                                    GATGAGAAACGAAAAGAATATGTCATCGGAGAGCTCATCTGGAATTTTGCTGACTTCATG
                                                 ACGAACCAGTCACCACTGAGAGTAACAGGAAACAAGAAGGGGGATCTTCACTCGACAGAGA
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Search completed: September 2, 2005, 00:30:40
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Compugen Ltd
     Aaa07937 Thermotog
Ads48252 Bacterial
Acn43424 Human dia
Acn43423 Human dia
Ab104147 Drosophil
Aad50922 L. mexica
Adf47502 Human bet
Adj58608 Fusion DN
Aad06386 Human bet
Add29602 Human cDN
Add29602 Human cDN
Add29602 Human bet
Abk83935 Cancer de
Acf57506 Human bet
Adj62864 Human bet
Adj62864 Human bet
Adj62864 Human bet
Adg89395 Cancer de
Acf57574 Mutant he
Aaf57574 Mutant he
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Aag58896 Humanised
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Adr16848 Arabidops	ADR16848	13	2001	6.6	110.8	45
Abkl5667 Glutathio	ABK15667	Q	2001	•	•	44
Aad19830 Beta-gluc	AAD19830	4.	2001	•	•	43
Ads46099 Bacterial	ADS46099	13	1812	6.6	110.8	42
Acc44709 E. coli b	ACC44709	10	1812	6.6	•	41
Abt16606 Artificia	ABT16606	œ	1812	6.6	•	40
Ab161371 GUS DNA #	ABL61371	σ	1812	٠	•	39
Aad29543 uidA DNA	AAD29543	თ	1812	6.6	•	38
Aah22503 PCR gener	AAH22503	4	1812	•	110.8	37
Abk87080 uidA DNA	ABK87080	σ	1809	6.6	110.8	36
Acc44712 Plasmid p	) ACC44712	10	14627	6.7	114	35
Ō.	ABT16610	æ	14627	6.7	114	34
Acc44711 Plasmid p	) ACC44711	10	3451	6.7	114	ü
Abt16609 Artificia	ABT16609	æ	3451	6.7	114	32
Adc01686 Enterohae	) ADC01686	10	1814	6.7	114	32
Aaa07938 Codon-opt	AAA07938	w	1888	7.7	130.4	30
Aaa07939 Salmonell	AAA07939	ω	1812	7.9	132.6	29
Aaa07958 Staphyloc	AAA07958	ω	1820	7.9	133	28
	AAX23826	N	1887	8.4	141.4	27
Acf64437 Propionib	ACF64437	œ	23078	8.4	142.2	26
Aas59508 Propionib	AAS59508	4	23078	8.4	142.2	25
Adg76418 Human Inc		10	2109	•	145.8	24
Acn43422 Human dia	ACN43422	13	1929	8.6	145.8	23
Aad06387 Murine be	AAD06387	4.	1947	9.4	159.6	22
Adb52752 Primary r	) ADB52752	10	2472	9.9	166.8	21

## ALIGNMENTS

AAA07937 standard; DNA; 1689

₽P.

Microbial; beta-glucoronidase; GUS; Enterobacter; Salmonella; Pseudomonas; Staphylococcus; Thermotoga; transgenic plant; bioindicator; transgenic insect; marker; glucuronide detoxification; ds. AAA07937; Jefferson RA, 21-SEP-2000. Thermotoga maritima. Thermotoga maritima beta-glucoronidase gene 17-MAR-1999; WO200055333-A1. 26-JAN-2001 16-MAR-2000; 2000WO-US007107. (CAMB-) CAMBIA BIOSYSTEMS LLC. (first entry) Mayer JE; 99US-00270957.

Novel microbial beta-glucuronidase genes and gene products used as reporter/effector molecule, as diagnostic tool, in positive selection, target molecules to specific cells and to detect and track linked genes. ť

Claim 2; Fig 4; 116pp; English.

WPI; 2000-647075/62. P-PSDB; AAB28406.

The present sequence encodes a microbial beta-glucuronidase (GUS) protein. GUS genes were obtained from six different genera: Enterobacter/Salmonella, Pseudomonas, Salmonella, Staphylococcus and Thermotoga. Microbial GUS can be used as a reporter/effector molecule for transgenic constructions and in in vitro diagnostic applications. It may also be used to generate sentinel plants that serve as bioindicators of

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Best Local Similarity
Matches 1689; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  environmental status. It may be used to generate transgenic insects for tracking insect populations or to facilitate the development of a bioassay for compounds that affect molecules critical for insect development (e.g. juvenile hormone). Secreted GUS may also serve as a marker for beneficial fungi destined for release into the environment. In animal systems, secreted GUS may be used to achieve extracellular detoxification of glucuronides (e.g. toxin glucuronide) and to examine conjugation patterns of glucuronides. Microbial GUS may also be used in traditional medical diagnostic assays, for drug testing, pharmacokinetic studies, bioavailability studies, diagnosis of diseases and syndromes, following progression of disease or its response to therapy. Microbial GUS has increased thermal stability, high turnover number and enzymatic activity. It is highly specific for the substrate and water soluble, and the substrates are stable
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                                                                            TTCGTCGAAGGGGAGTTCATCCTCGAAAACGCCAGGTTCTGGAGCCCTCGAAGATCCATAT
                                                                                                                                                                                GAACCGGAGAAGAAACTTGGAAAAGTGAAAGTGAAGATAGAAGTCTCAGAAGAAGCGGTG
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                            CTTTATCCTCTCAAGGTGGAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGA
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                                                                                                           Query Match
Best Local S
Matches 1688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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Pitts SC, Reddy TP;
Cerstin
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                                      Stuve LL;
UA, Kirto
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Sequence

2050 BP; 465 A; 532 C; 598 G; 455 T; 0 U; 0 Other;

Length 2050;

Similarity

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human conditions to diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorder, endocrine confections caused by virus, bacteria, fungi or parasite. The dithp confections caused by virus, bacteria, fungi or parasite. The dithp confecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp polynucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page; 190pp;
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P-PSDB; ABM84772.
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Query Match Best Local Simi Matches 493; 1295 1214 1235 1154 1175 1094 1115 1037 1055 1343 1274 977 995 917 935 875 815 737 797 CAGACAAGGGGGCTCCGTATGTGGATGTGATCTGTTTGAACAGCTACTACTTGGTATC GAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACA TGGATCGAACACGCCCCGTTGTCATGGTGAGCATGATGGACGCACCAGACGAGAGAACAA AGTCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCCTTTATGAGACTGCCAATGAAA CGCTGCCGCAGTTCTTCAACAACGTTTCTCTGCATCACCACATGCAGGTGATGGAAGAAG CAAGGTACCA---CTACAATCCCGAGACTCAGAAGATAGCAGAAGACAACATAAGAAGAA TGCAGATGTGTGACCGCTATGGGATTGTGGTCATCGATGAGTGTCCCGGCGTGGGCCTGG regarentecegaeaereegaareetregaaraeaegaaeeeeeeeeaeerregaatea 1036 TTCGCTGGCTTGGTGCCAACGCTTTCCGTACCAGCCACTACCCCTATGCAGAGGAAGTGA TGAAGTGGATCAACGCGAATTCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGC AGAGCCAGTTCCTCATCAATGGGAAACCTTTCTATTTCCACGGTGTCAACAAGCATGAGG AGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGCTTTGGAAAGCACGAGG TGGGGCCTGTGTCTGACTTCTACACACTCCCTGTGGGGATCCGCACTGTGGCTGTCACCA TGGAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGAACGATCAGCTGGGACG CGTCCCACCTAGAATCTGCTGGCTACTACTTGAAGATGGTGATCGCTCACACAAAATCCT TGGTGCGTAGGGACAAGAACCACCCCGCGGTCGTGATGTGGTCTGTGGCCAACGAGCCTG ATGCGGACATCCGAGGGAAGGGCTTCGACTGGCCGCTGCTGAAGGACTTCAACCTGC AATTCCCCGTTCTGGGGCAGGGCACCTTTATCCATTGATGATAAAAGACTTCAACCTTC Conservative 10.3%; .. Score 174; DB 13; Pred. No. 2.7e-43; 0; Mismatches 430; Indels 21; Gaps 1333 1093 1054 1402 1273 1213 1234 1174 1114 994 916 934 856 874

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human
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TTCACCAGGATCCACCTCTGATGTTCACTGAAGAGTACCAGAAAAGTCTGCTAGAGCAGT
                                                                                                           ATGCAAGGCACAGAAAGCCCATCTTTGTCACAGAATTCGGTGCGGACGCGATAGCTGGCA 1453
                                                                                                                                                                                   TCTATCAGGGAAGGATAGAAGAAGGACTTCAAGCTCTGGAAAAAGACATAGAAGAGCTCT
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                                                                        ATAAGAAGTATCAGAAGCCCATTATTCAGAGCGAGTATGGAGCAGAAACGATTGCAGGGT
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                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic a
genes from Drosophila
interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 6923; 21pp + Sequence Listing; English.
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11-JUL-2000; 2000US-00614150.
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TCTTTACAAGGAACCGACAACCCAAAGAAGTGGCTCACATTCTTAGGCGGCGGT
                                                                                                                CCTTTGCAGATTTTAAGACTCCTCAGAATGTGAGAAGACCCATTCTCAACCACAAGGGTG
                                                                                                                                                                      GGGATAGGTTCGGAAAĞCCTGTCATCCAATTTGAGTACGGCGGCGACACTATGGAGGGCA
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                                          TTTTCACAAGAGACAGACAACCCAAACTCGTTGCTCATGTACTGAGAAGACTGT
                                                                                    ACTTCGCCGATTTTCGGACCGCGCAGACTATTACCCGCGTGGGCGGCAACAAAAAGGGAG
                                                                                                                                                                                                                                                          TGCACTCACTTCCCCGCCTTTATTTGGTCGGAGGAATACCAGGTTGAGCTCTTCTCTCGCC
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AAD50922 standard; DNA; 2169 ВP

02-APR-2003 (first entry)

mexicana SAP-human beta-GUS-IGF-II chimeric DNA.

RESULT 6
AAD50922
ID AAD5
XX
AC AAD5
XX
DT 02-A
XX
DE L. m
XX
KW Lyso
KW Gauc
KW Niem
KW Niem Lysosome; metabolic disease; lysosomal storage disease; gene therapy; Gaucher's disease; Pompe's disease; Hurler's syndrome; neuroprotective; Niemann-Pick's disease; Schindler's disease; mucolipidosis; cystinosis; Batten's disease; prosaposin; infantile neuronal ceroid lipofiscinosis;

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                                                                        SXCCCCCCCCCCCXSXTTTTTXXRRXTXAXRRRRXTXTTTTTTTTTTTTTTXXSSSSXXXX
                               Query Match
Best Local Similarity
Matches 493; Conser
                                                                                                                              The invention relates to targetted therapeutic comprising a therapeutic agent that is active in a mammalian lysosome, and a means for binding an extracellular domain of human cation-independent mannose-6-phosphate receptor in a mannose-6-phosphate independent manner. The invention is useful for treating metabolic diseases such as lysosomal storage disease, e.g. Gaucher's disease, Pompe's disease, Hurler's syndrome, Niemann-Pick's disease, mannosidosis, fucosidosis, Schindler's disease, mucolipidosis, cystinosis, Batten's disease, prosaposin, or infantile neuronal ceroid lipofiscinosis. The invention is also useful in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
Leishmania me
Unidentified.
                                                                                                                                                                                                                                                                  New targeted therapeutic that is active in a mammalian lysosome binds extracellular domain of human cation-independent mannose-6-phosphate receptor, useful for treating metabolic diseases such as lysosomal
                                                                                         therapy. The present sequence is a DNA encoding Leishmania mexicana secreted acid phosphatase (SAP) signal peptide, human mature beta-Glucoronidase), linker and IGF-II chimeric protein. This sequence used in the exemplification of the invention
                                                                                                                                                                                                                                                          receptor, useful storage disease.
                                                                                                                                                                                                                                                                                                                                                                                 30-APR-2001; 2001US-0287531P.
10-JUL-2001; 2001US-0304609P.
15-OCT-2001; 2001US-0329461P.
23-JAN-2002; 2002US-0351276P.
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                                                                      Sequence
                                                                                                                                                                                                                                     Example 1; Fig 3; 68pp;
                                                                                                                                                                                                                                                                                                             P-PSDB;
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chimeric; gene; ds.
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DB; AAE33322.
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1807. .1815
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Pred. No. 2.8e-43;
D; Mismatches 430
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CC an extracellular domain of human cation-independent mannose-6-phosphate CC an extracellular domain of human cation-independent mannose-6-phosphate CC (M) is changed from isoleucine to threonine; and (i) binds the mutein CC with dissociation constant at least ten times the dissociation constant (CC with dissociation constant at least ten times the dissociation constant (CC for binding CM, Also described: (1) an underglycosylated therapeutic for binding CM, Also described: (1) an underglycosylated therapeutic CC fusion protein (FP) comprising a therapeutic domain and a subcellular can exterior surface of a cell, and upon internalisation of the receptor on can exterior surface of a cell, and upon internalisation of the receptor, compartment where the therapeutic domain to a subcellular compartment where the therapeutic domain to a subcellular compartment where the therapeutic domain to a subcellular compartment where the therapeutic domain to a subcellular compartment where the therapeutic domain to a subcellular compartment where the therapy and gene therapy. The P can be used in caryme replacement therapy, cell therapy and gene therapy. The P can be used for treating a patient by administering FP to the patient. GT can be used for treating a patient by identifying a caryment synthesising GT comprising a therapeutic agent that is therapeutic agent that is therapeutic agent that is compared to the patient, where the targeting moiety is dentified by screening a nucleic acid or peptide library. GT is useful for treating moiety disease, Gaucher disease, Krabbe disease, Schindler disease, Hurler constant engagement of the sease, Batten disease, Schindler disease, infantile carid storage disease. Batten disease, Schindler disease, infantile carid acroad disease. Batten disease.
sialic acid storage disease, Batten disease, infantile neuronal ceroid lipofuscinosis, Ehlers-Danlos syndrome type VI and congenital disorders of glycosylation. The present sequence is used in the exemplification o
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05-JUN-2002; 2002US-0386019P.
06-SEP-2002; 2002US-0408816P.
16-OCT-2002; 2002US-00272531.
06-FEB-2003; 2003US-0445734P.
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10-JUL-2001;
15-OCT-2001;
23-JAN-2002;
30-APR-2002;
29-MAY-2002;
05-JUN-2002;
06-SEP-2002;
              The invention relates to a targetted therapeutic which comprises a therapeutic agent that is active in a mammalian lysosome and means for binding an extracellular domain of human cation-independent mannose-6-phosphate receptor in a mannose-6 phosphate-independent manner. The targetted therapeutic, therapeutic fusion protein and methods of the invention are useful for treating lysosome storage diseases. The invention is also useful in gene therapy. The present sequence is a fusion DNA used in the exemplification of the invention. This DNA encor a fusion protein which comprises a signal peptide sequence, a human mature beta-glucoronidase (GUS) sequence, a bridge of three amino acids
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D; Mismatches 430
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Best Local Sim
Matches 492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of recombinant adeno-associated virus, comprising gene enco protein defective or missing in lysosomal storage disease, in t manufacture of a medicament for treating the lysosomal storage
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 1956 BP; 437 A; 533 C; 563 G;
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TGAAGTGGATCAACGCGAATTCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGC
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                                                                           AATTCCCCGTTCTGGGGCAGGGCACCTTTTATCCATTGATGATAAAAGACTTCAACCTTC
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                                                                                                                                                                                                                                                                                                                   TCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAGCTCGTTGAAAAG- 1512
                                                                                                                                                                                                                                                                                                                                                                        ATAAGAAGTATCAGAAGCCCATTATTCAGAGCGAGTATGGAGCAGAAACGATTGCAGGGT
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  TCACAAGAGACAGACAACCCAAACTCGTTGCTCATGTACTGAGA
                                                       TTGCCGATTTCATGACTGAACAGTCACCGACGAGAGTGCTGGGGAATAAAAAGGGGATCT
                                                                                                       TTGCAGATTTTAAGACTCCTCAGAATGTGAGAAGACCCATTCTCAACCACAAGGGTGTTT
                                                                                                                                                            ACCATCTGGGTCTGGATCAAAAACGCAGAAAATATGTGGTTGGAGAGCTCATTTGGAATT
                                                                                                                                                                                                               ACGATCAGGCTCCTTTTGAAAAAA----AGACTACATCATCGGAACACACGTGTGGGCCT
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                                                         1825
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RESULT 10 ABK83932 ID ABK83932 standard; cDNA; 2191 BP XX

Human cDNA differentially expressed in granulocytic cells #503

(first entry)

Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.

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                                                                                                                                                                                                                                                                       CC DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where CC differential expression of Gs is indicative of GCA. Also included are CC expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a CC tissue, an altergic response in a subject, exposure of a subject to a CC pathogen or sterile inflammatory disease using the gene expression of the gene is indicative of Grant the level of CC expression in a sample of the tissue of gene (s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating CC (M5) an inflammation (especially chronic) in a tissue, an altergic response in a subject to a pathogen or sterile inflammatory disease, by detecting the level of cof expression of the gene is indicative of inflammation; (4) treating CC (M5) an inflammation (especially chronic) or in a tissue, an altergic response in a subject, exposure of a subject, an altergic creponse in a subject, exposure of a subject to a pathogen or sterile inflammation of the gene (s) from Gs in the tissue. M1 (c) is useful for detecting GCA, M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an C1 inflammation in a tissue, an allergic response in a subject, capable of modulating GCA preferably in an C2 (especially chronic) in a tissue, an allergic response in a subject, caposure of a subject, a pathogen or sterile inflammatory disease (e.g. C2 postially chronic) and m1 useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, caposure of a subject, a pathogen or sterile inflammatory disease (e.g. C2 postially chronic) and m1 useful disease; also bacterial inflammation in a fissue, an altergic response in a subject, capable of m2 postial disease. C2 postial disease (e.g. C2 postial disease) crohn's capable of m2 postial disease (e.g. C2 postial diseas
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Best Local Sim
Matches 492;
                                                                                                                                                                                                                                                                  Sequence 2191 BP; 497 A; 589 C; 630 G; 475 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to detecting (M1) granulocyte (GC) activation
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                                    857
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                                                                                                                                                                                                                       Similarity
                                                                                          AGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGCTTTTGGAAAGCACGAGG
                             AATTCCCCGTTCTGGGGCAGGGCACCTTTATCCATTGATGATAAAAGACTTCAACCTTC
                                                                                                                                   TGGGGCCTGTGTCTGACTTCTACACACTCCCTGTGGGGATCCGCACTGTGGCTGTCACCA
                                                                                                                                                                    TGGAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGAACGATCAGCTGGGACG
  ATGCGGACATCCGAGGGAAGGGCTTCGACTGGCCGCTGCTGGTGAAGGACTTCAACCTGC
                                                                   AGAGCCAGTTCCTCATCAATGGGAAACCTTTCTATTTCCACGGTGTCAACAAGCATGAGG
                                                                                                                                                                                                                    10.2%;
                                                                                                                                                                                                                   Score 172.4; DB Pred. No. 9e-43;
                                                                                                                                                                                                     Mismatches
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RESULT 11
ADD29602
ID ADD29
XX
AC ADD29
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DT 15-JA
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DE Human
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DS Homo
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  31-DEC-2002; 2002WO-US041825
                                                                                                                                  ss; human; tumour
                                                                   WO2003058201-A2
                                                                                                Homo sapiens
                                                                                                                                                               Human tumour suppressor mRNA
                                                                                                                                                                                                    15-JAN-2004
                                                                                                                                                                                                                                   ADD29602;
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TCACTCGGCAGAGACAACCAAAAAGTGCAGCGTTCCTTTTGCGA 1895
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  suppressor; cancer; cancer;
                                                                       NO:55
  cytostatic;
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gene
therapy
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TGGATCGAACACGCCCCGTTGTCATGGTGATGATGGACGACGACGACGAGAGAACAA
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                                                  CGTCCCACCTAGAATCTGCTGGCTACTACTTGAAGATGGTGATCGCTCACACCAAATCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO
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18-SEP-2002;
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The invention relates to a method of predicting clinical outcome f patient diagnosed with cancer by determining the expression level or more genes, or their expression products, selected from p53BP2, cathepsin B, cathepsin L, Ki67/MiB1, and thymidine kinase in a car tissue obtained from the patient, normalized against control gene compared to the amount found in a reference cancer tissue set. The

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Disclosure;

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                                                   The present invention relates to a polypeptide comprising an CC antiangiogenesis polypeptide region linked to a therapeutic protein or polypeptide region, or a diagnostic protein or polypeptide region. The polypeptide comprising an antiangiogenesis polypeptide region or the nucleic acid encoding the polypeptide comprising the antiangiogenesis polypeptide region or the polypeptide is useful for diagnosing or treating angiogenesis-dependent cc diseases or cancer. Angiogenesis-dependent diseases include age-related macular degeneration, artherosclerosis, angiofibroma, neovascular cc glaucoma, arteriovenous malformations, nonunion fractures, arthritis, cc syndrome, psoriasis, corneal graft neovascularisation, pyogenic granuloma, delayed wound healing, retrolental fibroplasia, diabetic retinopathy, scleroderma, granulations, haemangioma, trachoma, haemophilic joints, vascular adhesions, hypertrophic scars, multiple sclerosis, restenosis or obesity. The present sequence is a coding sequence shown in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide comprising an antiangiogenesis polypeptide region linked to a therapeutic protein or a diagnostic protein, useful for diagnosing or treating angiogenesis-dependent diseases e.g. cancer, lupus or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein targeting; angiogenesis inhibitor; fusion gene; cancer; gene antiangiogenic; cytostatic; ophthalmological; antiarthritic; antirheumatic; antiinflammatory; dermatological; immunosuppressive; antipsoriatic; antidiabetic; neuroprotective; vasotropic; anorectic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
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CC This invention relates to a novel viral vector comprising a beta-
CC catenin/bipartite T-cell factor (Tcf)-responsive promoter construct which
CC contains a first promoter region having a copy of Tcf/LEF-1 binding site
CC operatively linked to a second promoter region, and a nucleic acid
CC sequence, where the first and second promoter regions are operatively
CC linked to target nucleic acid sequence. The invention may be useful for
CC the development of compounds with a cytostatic activity, through action
CC as beta-catenin activity inhibitors, or for gene therapy. The invention
CC may be useful for treating an individual with colon cancer which is
CC metastasised to the liver. The treatment involves administering the
CC vector of the invention where the nucleic acid sequence encodes a
CC therapeutic polypeptide or thymidine kinase, a prodrug and chemotherapy,
CC radiation, surgery or gene therapy to the individual. The present
CC sequence is that of a therapeutic gene which may be used in the vector of
CC the invention for the treatment of an individual with cancer.
Query Match
Best Local Sim
Matches 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel viral vector comprising beta-catenin/bipartite T-cell factor-responsive promoter having first and second promoter region linked target nucleic acid sequence, useful for treat- ing colon cancer.
                                                                         Sequence 2191 BP; 497 A; 589 C; 630 G; 475 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 16; 114pp; English.
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Score 172.4; DB Pred. No. 9e-43; 0; Mismatches 4
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The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosis and monitoring of allograft rejection and other disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing or monitoring transplant rejection, e.g. heart, kidney, live pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level
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5 밁 S Matches 492; Query Match Sequence 2191 BP; 497 A; 589 C; 630 G; 475 T; 0 U; 0 Other; Match 10.2%; Local Similarity 52.1%; TGGAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGAACGATCAGCTGGGACG AGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGCTTTGGAAAGCACGAGG TGGGGCCTGTGTCTGACTTCTACACACTCCCTGTGGGGATCCGCACTGTGGCTGTCACCA Conservative Score 172.4; DB 12; Pred. No. 9e-43; 0; Mismatches 431; Indels Length 21; Gaps 1023 796 856

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Search completed: September 1, 2005, 22:25:44 Job time : 985 secs

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## ALIGNMENTS

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REFERENCE
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 215
                                                                                                                                                                                                                                                                                                                                             Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1377)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Fill-length cDNA libraries and normalization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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TGGGGCCTGTGTCTGACTTCTACACACTCCCTGTGGGGATCCGCACTGTGGCTGTCACCA 274
                                   TGGAACTTGAAAAAGACGAGTACACTCTGGACATCGGAATCAGAACGATCAGCTGGGACG 796
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                                                                                Conservative
                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSODL001YM21"
/tissue_type="B_cells (Ramos cell line) Cot 25-normalized"
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                 10.3%;
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                                                                           Score 174; DB Pred. No. 7.7e-0; Mismatches
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Hawkins, P.R.,

splice variant Chien, D.,

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Homo sapiens (human)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Contact: Jin, P.
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Jin,P., Fu,G.K., Wilson,A.D., Yang,
Au-Young,J. and Stuve,L.L.
PCR isolation and cloning of novel
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Fax: 650 621 8965
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Single gene library"
/note="Vector: pDrive Cloning Vector; RT-PCR was performed using gene-specific primers flanking the open-reading frame. PCR products were subcloned into pDrive Cloning Vector and sequenced completely using M13 forward and reverse primers. Sequencing gaps were closed by re-sequencig using primers flanking the gapped areas."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1995)
Jin,P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R.,
Au-Young,J. and Stuve,L.L.
PCR isolation and cloning of novel splice variant mRNAs from k
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Genomics 83 (4), 566-571
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AATTCCCCGTTCTGGGGGCAGGGCACCTTTATCCATTGATGATAAAAGACTTCAACCTTC
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Location/Qualifiers
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/note="Vector: pDrive Cloning Vector; RT-PCR was performed /note="Vector: pDrive Cloning Vector; RT-PCR was performed using gene-specific primers flanking the open-reading frame. PCR products were subcloned into pDrive Cloning Vector and sequenced completely using M13 forward and reverse primers. Sequencing gaps were closed by re-sequencig using primers flanking the gapped areas."
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/db_xref="taxon:9606"
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Kingsley, D.M., Peichel, C., Balabahdra, S., Schmutz, J. and Myers, R.M.
Expressed sequence tags from Gasterosteus
                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.

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                                                                                                                                                     Gasterosteus aculeatus (three spined stickleback) Gasterosteus aculeatus
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HHMI and Department of Developmental Biology
Stanford University School of Medicine
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Email: kingsley@cmgm.stanford.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: lambda ZAP Express/pBK-CMV; Site 1: EcoR1 (5' adaptor); Site 2: XhoI (3' linker primer); The mixed organ cDNA library was generated using the ZAP-cDNA method by Stratagene. First strand cDNA synthesis was primed with a 50 bp linker primer containing an oligo dT sequence preceded by a synthetic XhoI site. 5 prime adaptors were used containing an EcoR1 cohesive end. The finished cDNAs were inserted in to the ZAP express vector unidirectionally in the sense orientation with respect to the lacZ promoter of pBK-CMV. An amplified library was prepared from approximately 3 million primary clones in the lambda ZAP Express vector. In vivo excision was then used to generate individual pBK-CMV phagemid clones for EST sequencing."
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/strain="Salinas river,
/db_xref="taxon:69293"
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/tissue_type="heads and internal organs
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Gasterosteus aculeatus (three spined stickleback)
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1 (bases 1 to 1138)
Balabahdra, S., Grimwood, J., Dickson, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kingsley, DM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kingsley,D.M., Peichel,C., Balabahdra,S., Schmutz,J. and Myers,R.M.
Expressed sequence tags from Gasterosteus Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                   quality sequence
                                                                                                                                                                                                                                                                                                                                                                                             kingsley@cmgm.stanford.edu
/sex="mixed male and female"
/tissue_type="heads and internal organs combined"
/dev_stage="adult"
/clone_lib="SHGC-CDA"
/note="Vector: lambda ZAP Express/pBK-CMV; Site_1: EcoRl
(5' adaptor); Site_2: XhoI (3' linker primer); The mixed
organ cDNA library was generated using the ZAP-cDNA method
by Stratagene. First strand cDNA synthesis was primed with
a a 50 bp linker primer containing an oligo dT sequence
                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="Salinas river,
/db_xref="taxon:69293"
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                    clone="CDA60-D07"
                                                                                                                                                                                                                                                                                     organism="Gasterosteus aculeatus"
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AGACTCCTCAGAATGTGAGAAGACCCATTCTCAACCACAAGGGTGTTTTCACAAGAGACA
                                                                                                                                                                                                                                                                                                                AGAAAGCCCATCTTTGTCACAGAATTCGGTGCGGACGCGATAGCTGGCATCCACTACGAT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACATCTATCAGGGA 1344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCCCTACGTGGACGTCATCTGCGTAAACAGTTACTTCTCCTGGTACCATGACCCGGGC 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGCCCGT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCCCCGTTGTCATGGTGAGCATGATGGACGCACCAGACGAGAGAACAAGAGACGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTCCTGCTGATTACTATTTCAAAACCTTGATAAAACATACCAAAGAATTGGATCCAACC
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                                                                                                                                                                             CCACCCGTGATGTTTACTGAGGAGTACCAGAAGTTAGTCCTGCAGAGCTACCACAACGTG
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                                                                                                                              CTTTTGAAAAAG----ACTACATCATCGGAACACACGTGTGGGCCTTTGCAGATTTTA
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                  Rogabe, Y., Saito, R., Natimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                            Group Phase I & II Team.

Analysis of the mouse transcriptome of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases I 20274)
Submitted (16-JUL-2001) Yoshihide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus adult male aorta and vein cDNA, RIKEN full-lengtlenriched library, clone:A530072005 product:beta-glucuronidase etructural, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The FANTOM Consortium and the RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Please visit our web site for further details.
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/clone_Tib="RIKEN full-length enriched mouse cDNA library"
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Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L.
Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library embryos representing early developmental stages
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CK467358.1
EST.
                                                                                                                                                                                           Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called
trimmed with the aid of the trim_alt
cross_match_v0.990329.
Plate: TMW8042 row: M column: 18
Seq_primer: GTAATACGACTCACTATAGGG.
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Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   938649 MARC 4PIG Sus scrofa cDNA
                                                                                                                                                                                                                                                                                              USDA, ARS, US Meat Animal PO Box 166, Clay Center, N Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                 Contact: Smith TPL
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Mammalia; Eutheria;
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            /clone lib="MARC 4PIG"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site
Library made with combined RNA from day-10, d
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                                                                                                          organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
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'lab_host="DH10B"
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Matches 396;
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AGENCOURT_8741562 NIH_MGC_18
5', mRNA sequence.
8Q941196
BQ941196.1 GI:22356674
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 906)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collect Unpublished (1999)
                                                                                                                                          Homo sapiens
                                                                                                                                                               Homo sapiens (human)
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Best Local Similarity 52.1
Matches 454; Conservative
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://image.llnl.gov
Plate: LLCM2594 row: g column: 16
High quality sequence stop: 765.
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     GCAGCTGGCCACCCAGTTTGAGAACTGGTATAAGAAGTATCAGAAGCCCATTATTCAGAG
                                                                                                                  CGTGATGTGGTCTGTGGCCAACGAGCCTGCGTCCCACCTAGAATCTGCTGGCTACTACTT
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                                            AGCTCTGGAAAAAGACATAGAAGAGCTCTATGCAAGGCACAGAAAGCCCCATCTTTGTCAC 142
                                                                                                                                                                                   CAACTCTAACTATGCAG------CAGACAAGGGGGCTCCGTATGTGGATGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_18"
/clone
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6420519"
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Pred. No. 4.5e-31;
0; Mismatches 396;
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Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phi
trimmed with the aid of the trim_alt option.
cross_match v0.990329.
Plate: TMW8046 row: I column: 19
Seq primer: GTAATACGACTCACTATAGGG.
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Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library compression of the complex of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collection of the collecti
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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Contact: Smith TPL
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
        TCAACGCGAATTCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGCTGGATCTTG
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/lab_host="DH10B"
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E 1 (bases 1 to 1051)

S Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

L Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30372720.

Contact: Genoscope

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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five
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BX363460 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL001YM21 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCGGCCCGTGACCTTCGTGACCA-----GCTCCAGCTATGA----AAAAGACCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCCAGACGCGGAGGGTTTCTTCAAAGCCCTTTATGAGACTGCCAATGAAATGGATCGAA 1222
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                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODLOOIAG11QP1&c=4169.r. Location/Qualifiers
ATGCAAGGCACAGAAAGCCCCATCTTTGTCACAGAATTCGGTGCGGACGCGATA-GCTGGC 1452
                                                                                                                                                           GAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACA 1333
                                                                                                                                                                                                                                                                                                    AGTCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCCTTTATGAGACTGCCAATGAAA
                                                                                                                                                                                                                             TGGATCGAACACGCCCCGTTGTCATGGTGAGCATGATGGACGCACCAGACGAGAGAACAA 1273
                                                                                                                                                                                                                                                                  CGTCCCACCTAGAATCTGCTGGCTACTACTTGAAGATGGTGATCGCTCACACCAAATCCT
                                                                                                                                                                                                                                                                                                                                                                CGCTGCCGCAGTTCTTCAACAACGTTTCTCTGCATCACCACATGCAGGTGATGGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAGGTACCA---CTACAATCCCGAGACTCAGAAGATAGCAGAAGACAACATAAGAAGAA 1093
                                                      TCTATCAGGGAAGGATAGAAGAAGGACTTCAAGCTCTGGAAAAAGACATAGAAGAGCTCT
                                                                                                                         CAGACAAGGGGGCTCCGTATGTGGATGTGATCTGTTTGAACAGCTACTACTCTTGGTATC
                                                                                                                                                                                             TGGACCCCTCCCGGCCTGTGACCTTTGTGAGCAACTCTAACTATGCAG--------
                                                                                                                                                                                                                                                                                                                                      TGGTGCGTAGGGACAAGAACCACCCCGCGGTCGTGATGTGGTCTGTGGCCAACGAGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="Homo sapiens B CELLS (RAMOS CELL LINE) 25-NORMALIZED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="CSODLOO1YM21"
/cell_type="B CELLS (RAMOS CELL LINE)
/cell_line="RAMOS CELL LINE"
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/mol_type="mRNA"
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Pred. No. 3.2e-30;
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Matches 386; Conserv
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Contact: Zoorob R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mdvn127 c10 r2 Marek's disease virus-infected spleen Gallus cDNA, mRNA sequence. CF255373 CF255373.1 GI:33488628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 33 1 49 58 35 00
Fax: 33 1 49 58 33 81
Email: zoorob@vjf.cnrs.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                 CTGAACGGGAAACCTGTCTTTTGAAGGGCTTTGGAAAGCACGAGGAATTCCCCGTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACGAGTACACTCTGGACATCGGAATCAGAACGATCAGCTGGGACGAGAAGAGGCTCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCCACTACGATCCACCTCAAATGTTCTCCCGAAGAGTACCAAGCAGAGCTCGTTGAAAAG 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATAAGAAGTATCAGAAGCCCATTATTCAGAGCGAGTATGGAGCAGAAACGATTTGCAGGG
                                      GCAAACTCCTTCCGTACCAGCCACTACCCCTATGCTGAGGAGATCATGGACCTGTGTGAC
                                                                                                                                                                                                           GCGAATTCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGCTGGATCTTGCCGAC
                                                                                                                                                                                                                                                       GGCAAAGGCCTGGACTGGGCACTGATCGTTAAGGACTTCAACCTGCTGCGCTGGTTGGGG
                                                                                                                                                                                                                                                                                             GGGCAGGGCACCTTTTATCCATTGATGATAAAAGACTTCAACCTTCTGAAGTGGATCAAC
                                                                                                                                                                                                                                                                                                                                         ATCAACGGAAAGCCCTTCTACTTCCACGGGGTCAACAAGCACGACGACGCGCGGATATTCGT
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TTTGGGAACAAATCTCTACAGCATCATCTCGTCGTGATGGAGGAACTGATCCGCAGGGAT
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                                                                                 ACCTACGGCATTGTGGTGATCGACGAGTGCCCGGGCGTGGGGGATTAAGATGCCTGAGAGC
                                                                                                                       AGACTCGGAATCCTTGTGATAGACGAAGCCCCGCACGTTGGTATCACAAGG----TACCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone_lib="Marek's disease virus-infected
/note="Organ: Spleen; Vector: pTriplEX2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.98;
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Pred. No. 1.4e-27;
0; Mismatches 364;
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CA453907
CA453907.1 GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 846)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                             High
                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM14275 row: a column: 17
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AGENCOURT_10738557 MAPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D
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Homo sapiens
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Location/Qualifiers
                 /clone lib="MAPCL"
/note="Vector: pCMV-SPORT6; Site 1: ECORV; Site 2: Not I;
/note="Vector: pCMV-SPORT6; Site 1: ECORV; Site 2: Not I;
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/note="Vector: pCMV-SPORT6; Site 1: ECORV; Site 2: Not I;
/note="Vector: pCMV-SPORT6; Site 1: Note 2: N
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/mol_type="mRNA"
/db_xref="taxon:9606"
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11_line="ZR-75-1, MCF7,
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 CA489317.1
EST.
Homo sapiens
                                                                     mRNA sequence
CA489317
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                                                                                                                                                                                                                                                                                                                                                                TTCATGACTGAACAGTCACCGACGÁGAGTGCTGGGGAATTAAAAAGGGGATCTTCACTCG
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nilarity 52.4%;
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                                              GI:24952108
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Pred. No. 4.4e-27;
0; Mismatches 356;
                                                                                                                      Homo
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                                                                                                                    sapiens cDNA
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM14283 row: d column: 20
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1 (bases 1 to 900)
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                                      CGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACATCTATCAGG
                                                                                                                                                                                              TAGAATCTGCTGGCTACTACTTGAAGATGGTGATCGCTCACACCAAATCCTTGGACCCCT
                                                                                                                                                                                                                                                                                                                                 ATCCAGACGCGGAGGGTTTCTTCAAAGCCCTTTATGAGACTGCCAATGAAATGGATCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGACCGCTATGGGATTGTGGTCATCGATGAGTGTCCCGGCGTGGGCCTGGCGCTGCCGC
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6721700"
/cell_line="ZR-75-1, MCF7, ShTERT-HME1, LNCap"
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Pred. No. 1e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM0048 row: n column: 19
High quality sequence stop: 580.
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Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Contact: Robert Strausberg, Ph.D.
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AGENCOURT 11297304 NIH MGC 135 Mus musculus
IMAGE:30141354 5', mRNA sequence.
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                                                   /mol_type="mRNA"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:30141354"

/lab_host="DH10B (phage-resistant)"

/clone=lib="NIH_MGC_135"

/note="Vector: pCMVSport6.1; Site_1: EcoRV; Site_2: NotI;

/note="Vec
by, David 1
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                                      Rowe. Library constructed by ResGen, Invitrogen
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Query Match Best Local Similarity Matches 410; Conserv

Conservative

7.7%;

Score 129.8; DB 6; Pred. No. 1e-26; D; Mismatches 382;

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1 (bases 1 to 862)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                       Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                           CO394571 862 bp mRJ
AGENCOURT 27822917 NIH MGC 252 Rattus
IMAGE: 7307606 5', mRNA sequence.
                                                                                                                                                                        CO394571
CO394571.1 GI:49576487
                                                                                                                                  Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                   CAGCCCAAAACTTCGGCCTTTATTTTGCGAAGA 803
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cDNA Library Preparation: Express Genomics

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM15349 row: e column: 12
High quality sequence stop: 685.
Location/Qualifiers
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                                                         AATGGATCGAACACGCCCCGTTGTCATGGTGAGCATGATGGACGCACCAGACGAGAGAAC 127
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/note="Organ: ovary; Vector: pDONR 201; Site_1: NotI;
Site_2: NotI; RNA obtained from female overies animals at
8 wk old. Tissues were snap-frozen and kept at -80C for
two days before RNA extraction and purification
(Tri-reagent method). cDNA was primed using oligo-dT
primer: 5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and
cloned into the EcoRV/NotI sites of pExpress-1.
Size-selection >1.25kb resulted in an average insert size
of 1.7kb. This primary library is not normalized
(normalized library is NIH MGC 252) and was constructed by
Express Genomics (Frederick, MD). Note: this is a NIH_MGC
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Tissue was snap-frozen adn transferred in -70C. RNAse f
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b_host="DH10B TonA"
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1512 GACGATCAGGCTCCTTTTGAAAAAAGA 1538 	1452 CATCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAGCTCGTTGAAAA 1511	392 CTATGCAAGGCACAGAAAGCCCATCTTTGTCACAGAATTCGGTGCGGACGCGATAGCTGG 1451	1332 CATCTATCAGGGAAGGATAGAAGAAGAAGGACTTCAAGCTCTGGAAAAAGACATAGAAGAGCT 1391	272 AAGAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTA 1331

Search completed: September 2, 2005, 02:08:04 Job time : 5847 secs

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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ATAGAAGAGCTCTATGCAAGGCCACAGAAAGCCCCATCTTTGTCACAGAATTCGGTGCGGAC
                  ATAGAAGAGCTCTATGCAAGGCACAGAAAGCCCATCTTTGTCACAGAATTCGGTGCGGAC 1440
                                                                                       TACGGCTGGTACATCTATCAGGGAAGGATAGAAGAAGGACTTCAAGCTCTGGAAAAAGAC
                                                                                                                                         GACGAGAGAACAAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTAC
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Podsakoff, Gregory
APPLICANT: Watson, Gordon
APPLICANT: Watson, Gordon
APPLICANT: Couto, Linda B.
APPLICANT: Yang, Bin
TITLE OF INVENTION: TRECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS FOR
TITLE OF INVENTION: TREATMENT OF LYSOSOMAL DISORDERS
FILE REFERENCE: 0800-0021
CURRENT APPLICATION NUMBER: US/09/715,858
CURRENT FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1956
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1956)
US-09-715-858-1
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CGCTGCCGCAGTTCTTCAACAACGTTTCTCTGCATCACCACATGCAGGTGATGGAAGAAG
                             САЛБСТАССА---СТАСЛАТСССБАБАСТСАБАЛБАТАБСАБАЛБАСЛАСАТАЛБАЛБАЛ 1093
                                                                                                TGGATCTTGCCGACAGACTCGGAATCCTTGTGATAGACGAAGCCCCGCACGTTGGTATCA 1036
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Pred. No. 5.5e-43;
D; Mismatches 431;
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RESULT 3
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COUNTRY: USA
ZIP: 20007-5109
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,555B
FILING DATE: 16-MAR-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19710643.9
FILING DATE: 14-MAR-1997
FILING DATE: 14-MAR-1997
                                                                                                                                                                                                                                                                                                APPLICANT: Koerner, Kathrin
APPLICANT: Mueller, Rolf
APPLICANT: Sadlacek, Hans-Harald
TITLE OF INVENTION: PROMOTER OF THE CI
TITLE OF INVENTION: PREPARATION AND US
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2191 base pairs
TYPE: nucleic acid
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REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 0167
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
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TOPOLOGY: lir
MOLECULE TYPE:
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                      TCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAGCTCGTTGAAAAG-
                                                                                                                                                       TCTATCAGGGAAGGATAGAAGAAGGACTTCAAGCTCTGGAAAAAAGACATAGAAGACCTCT
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Matches 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09715858 Patent No. 6582692 GENERAL INFORMATION:
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APPLICANT: Couto, Linda B.
APPLICANT: Yang, Bin
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                                                                                                                                                                                       ACAAGGTACCACTACAATCCCGAGACTCAGAAGATAGCAGAAGACAACATAAGAAGATG
                                                                                                                                                                                                                                                               GATCTTGCCGACAGACTCGGAATCCTTGTGATAGACGAAGCCCCGCACGTTGG---TATC 1035
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TCTGCTCTGAAACCCCGCCGCATATTACTTTAAGACGCTGATCACCCACACCAAAGCCCCTG
                                  TCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCTTTATGAGACTGCCAATGAAATG 1215
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APPLICANT: Jefferson, Richard A.
APPLICANT: Kilian, Andrzej
APPLICANT: Kilian, Andrzej
APPLICANT: Kilian, Andrzej
APPLICANT: Keese, Paul Konrad
TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS:
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 190106.405
CURRENT APPLICATION NUMBER: US/09/149,727
CURRENT APPLICATION NUMBER: US/09/149,727
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: US 60/058,263
EARLIER FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.4%;
Best Local Similarity 45.4%;
Matches 734; Conservative
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; Patent No. 6641996
; GENERAL INFORMATION:
; APPLICANT: Richard A. Jefferson and Jorge E. Mayer
; TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GI
; TITLE OF INVENTION: PRODUCTS, AND USES THEREOF
; FILE REFERENCE: 190106.405C1
; CURRENT APPLICATION NUMBER: US/09/270,957
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 45.4%;
Matches 734; Conservative
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                                       TTGAAAAGACGATCAGGCTCCTTTTGAAAAAAAGACTACATCGTCGGAACACACGTGTGGG
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; STRANDEDNESS:
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; MOLECULE TYPE: D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application Patent No. 5830698 GENERAL INFORMATION:
APPLICANT: REFF, Mit
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                              Matches 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,866
FILING DATE: 14-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 14683 base pair
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: BARNETT, Richard Spence
APPLICANT: MCLACHLAN, Karen Retta
TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT
TITLE OF INVENTION: SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
TITLE OF INVENTION: RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Teskin, Robin L. REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: P.O. Box
CITY: Alexandria
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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r: United States
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  TCCTACCGTACCTCGCATTACCCTTACGCTGAAGAGATGCTCGACTGGGCAGATGAACAT 7109
                                                                                                          GGCACCTTTTATCCATTGATGATAAAAGACTTCAACCTTCTGAAGTGGATCAACGCGAAT
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                               TCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGCTGGATCTTGCCGACAGACTC
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P.O. Box 1404
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48.1%;
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                                                                                                                                                                                                                                                                                                               Score 112; DB 2;
Pred. No. 1.6e-23;
                                                                                                                                                                                                                                                                                              Mismatches 450;
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RESULT 8
US-09-023-715-1/c
                      APPLICANT: REFF, Mitchell E.
APPLICANT: BARNETT, Richard Spence
APPLICANT: MCLACHLAN, Karen Retta
TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT
TITLE OF INVENTION: SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
TITLE OF INVENTION: RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application Patent No. 5998144 GENERAL INFORMATION:
         READABLE
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         FORM:
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; LENGTH: 14683 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vc
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,715
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 14-MAR-1997
ATTORNEY/AGENT INFORMATION:
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GTCTGTGTGAACAGGTACTACGGCTGGTACATCTATCAGGGAAGGATAGAAGAAGGACTT
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                                                                                                                  AGCATGATGGACGCACCAGACGAGAGAACAAGAGACGTGGCGCTGAAGTACTTCGACATC
                                                                                                                                                                 TTCGCGCCACTGGCGAAGCAACGCGTAAACTCGACCCGACGCGTCCGATCACCTGCGTC
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SEQ ID NO 1
LENGTH: 14683
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09343485A Patent No. 6413777
                                                                                                                                                                                                                                                           Matches 472;
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: REFF, MITCHELL R.
APPLICANT: BARNETT, RICHARD S.
APPLICANT: MCLACHLAN, KAREN R.
TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES
TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
FILE REFERENCE: 037003-0275807
CURRENT APPLICATION NUMBER: US/09/343,485A
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/023,715
PRIOR APPLICATION NUMBER: 08/819,866
PRIOR APPLICATION NUMBER: 08/819,866
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description OTHER INFORMATION: referred to
                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                            CACAAACCGTTCTACTTTACTGGCTTTGGTCGTCATGAAGATGCGGACTTGCGTGGCAAA
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TCTTTCAGGACCTCTCACTATCCTTACAGTGAAGAGTGGCTGGATCTTGCCGACAGACTC
                                     GGATT CGATAA CGTGCTGATGGTGCACGACCACGCATTAATGGACTGGATTAGGGCCAAC
                                                                        GGCACCTTTTATCCATTGATGATAAAAGACTTCAACCTTCTGAAGTGGATCAACGCGAAT
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                                                                                                                                                                                                                                                        Score 112; DB 3;
Pred. No. 1.6e-23;
0; Mismatches 450
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                                                                                                                                                                                                                   Sequence 18, Application Patent No. 5861277 GENERAL INFORMATION:
                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rose, Alan B.
APPLICANT: Last, Robert L.
APPLICANT: COMPOSITIONS FOR ENHANCING TITLE OF INVENTION: THE EXPRESSION OF GENES IN PLANTS
NUMBER OF SEQUENCES: 21
                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WH
STREET: P.O. Box 4433
                                  CITY: Houston STATE: TX
 COUNTRY: U
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Best Local Similarity
Matches 465; Conserv
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 3035 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: BTIE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHONE: 512/474-7577
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: Concurrently CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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                                                                     GTCTGTGTGAACAGGTACTACGGCTGGTACATCTATCAGGGAAGGATAGAAGAAGGACTT
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                                   CTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGCGGCGATTTGGAAACGGCAGAG 2669
                                                                                                          AATGTAATGTTCTGCGACGCTCACACCGATACCATCAGCGATCT-----CTTTGATGTG
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Pred. No. 1.4e-23;
0; Mismatches 457;
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RESULT 11
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,820
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19513676.4
FILING DATE: 11-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS Datricia D
                                                                                                                                                               TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                          NAME: GRANADOS, PATRICIA D. REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 1874
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                 MOLECULE TYPE: cDI
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OPPER, Martin
APPLICANT: BOSSLET, Klaus
APPLICANT: CZECH, Joerg
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
TITLE OF INVENTION: IN E. COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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STREET: 3000 K SI
CITY: Washington
                                                                                            LENGTH: 3169 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
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IMMEDIATE SOURCE:
CLONE: pTrc99 dicistr.
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ATCATCGGAACACGTGTGGGCCTTTGCAGATTTTAAGACTCCTCAGAATGTGAGAAGA 1602
                                                                                GAAGAGTACCAAGCAGAGCTCGTTGAAAAGACGATCAGGCTCCTTTTGAAAAAAAGACTAC 1542
                                                                                                                                              ACAGAATTCGGTGCGGACGCGATAGCTGGCATCCACTACGATCCACCTCAAATGTTCTCC 1482
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                                                GAAGAGTATCAGTGTGCATGGCTGGATATGTATCACCGCGTCTTTGATCGCGTCAGCGCC
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LUCATION: 666..3162
; SEQUENCE DESCRIPTION: SEQ US-09-273-453-5
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US-09-273-453-5
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                                                                                                                                                                                                                                                                                                                                                      TELEX: 904136 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION UMBER: US/09/273,453
FILING DATE: 22-Mar-1999
PRIOR APPLICATION NUMBER: 08/630,820
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/630,820
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/306
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OPPER, Martin ROSSLET, Klaus
                                                                                                                                                          STRAIN: pRAJ210 IMMEDIATE SOURCE:
                                                                                                                                                                                         ORIGINAL SOURCE:
ORGANISM: Enterobacteriaceae:
                                                                                                                                                                                                                                     TOPOLOGY: circular MOLECULE TYPE: cDNA HYPOTHETICAL: NO
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                                            NAME/KEY: CDS
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TELEFAX: (202)672-5399
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                                                             GTTGGCGGTÄÄCAÄGÄÄÄAGGGATCTTCÄCTCGCGÄCCGCAÄÄCCGAÄGTCGGCGCTTTT
                                                                                         ATCATCGGAACACGTGTGGGCCTTTGCAGATTTTAAGACTCCTCAGAATGTGAGAAGA 1602
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                                                                                                                         GTCGTCGGTGAACAGGTATGGAATTTCGCCGATTTTTGCGACCTCGCAAGGCATATTGCGC
                                                                                                                                                                                      GAAGAGTATCAGTGTGCATGGCTGGATATGTATCACCGCGTCTTTGATCGCGTCAGCGCC
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0; Mismatches 457;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,624
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.6%;
Best Local Similarity 47.4%;
Matches 465; Conservative
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APPLICANT: Rose, Alan B.

APPLICANT: Last, Robert L.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING TITLE OF INVENTION: THE EXPRESSION OF GENES IN PLANTS NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE & DURKEE

STREET: P.O. Box 4433
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TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 3824 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 3824 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
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ZIP: 77210
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GTGATCATGTGGAGTGTGGCGAACGAACCAGAGTCCAACCATCCAGACGCGGAGGGTTTC 1182
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                                       CAGCAAGCGCACTTACAGGCGATTAAAAGAGCTGATAGCGCGTGACAAAAAACCACCCAAGC
                                                                           TTCGAAGCGGGCAACAAGCCGAAAGAACTGTACAGCGAAGAGGCAGTCAACGGGGAAACT
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Pred. No. 1.7e-23;
0; Mismatches 457;
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CURRENT APPLICATION NUMBER: US/09/893,525
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 09/210,843
PRIOR FILING DATE: 1998-12-15
PRIOR FILING DATE: 1997-04-25
PRIOR APPLICATION NUMBER: US 08/366,783
PRIOR FILING DATE: 1994-12-30
PRIOR APPLICATION NUMBER: US 08/142,418
PRIOR APPLICATION NUMBER: US 08/142,418
PRIOR APPLICATION NUMBER: US 07/659,835
PRIOR APPLICATION NUMBER: US 07/659,835
PRIOR FILING DATE: 1993-11-16
PRIOR APPLICATION NUMBER: US 07/659,835
PRIOR FILING DATE: 1991-02-22
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
LENGTH: 4652
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US-09-893-525-36
; Sequence 36, Application
; Patent No. 6753167
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phas-GUS-phas
; NAME/KEY: CDS
; LOCATION: (1548)..(3359)
; OTHER INFORMATION:
US-09-893-525-36
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APPLICANT: Van Rooijen, Gijs
TITLE OF INVENTION: Preparation of Heterologous Proteins on
FILE REFERENCE: 9369-172
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GENERAL INFORMATION:

APPLICANT: Moloney, Maurice M.

APPLICANT: Van Rooijen, Gijs

TITLE OF INVENTION: Preparation of Heterologous Proteins on Oil Bodi

FILE REFERENCE: 9369-172

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 09/210,843

PRIOR FILING DATE: 1998-12-15

PRIOR APPLICATION NUMBER: US 08/846,021

PRIOR APPLICATION NUMBER: US 08/846,021

PRIOR APPLICATION NUMBER: US 08/846,783

PRIOR FILING DATE: 1997-04-25

PRIOR APPLICATION NUMBER: US 08/366,783

PRIOR APPLICATION NUMBER: US 08/142,418

PRIOR APPLICATION NUMBER: US 08/142,418

PRIOR APPLICATION NUMBER: US 08/142,418

PRIOR FILING DATE: 1993-11-16

PRIOR FILING DATE: 1993-11-16

PRIOR FILING DATE: 1991-02-22

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn version 3.1

SEQ ID NO 41

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; OTHER INFORMATION: phas-caleo-GUS-phas
; NAME/KEY: CDS
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                                                                                                   GTGATCATGTGGAGTGTGGCGAACGAACCAGAGTCCAACCATCCAGACGCGGAGGGTTTC 1182
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Search completed: September 1, 2005, 19:13:25 Job time : 340 secs Charles and state of

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
/ Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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/ Cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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/ Cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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/ Cgn2_6/ptodata/2/pubpna/US11N_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/US10I_NEW_PUB.seq:*
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  (without alignments)
9510.845 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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172.4	174	174	174	175.4	1688	1688	Score
10.2	10.3	10.3	10.3	10.4	99.9	99.9	Query Match
1956	2169	2169	2169	1926	1692	1689	Query Match Length DB ID
17	17	17	14	22	17	17	BB
US-10-421-175-1	US-10-272-483A-5	US-10-272-531A-5	US-10-136-841-5	US-10-757-093-1	US-10-369-493-26682	US-10-364-649-14	DB ID
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ion US/10364649 30229921A1 . Jefferson and Jorge E. Mayer MICROBIAL B-GLUCURONIDASE GENES,	ALIGNMENTS	10-239-	US-10-832-815-5 US-10-239-907A-49	10-239-907A	10-239-907A-	US-10-800-161-29	10-332-406A	US-10-239-907A-38	0 (	US-10-149-533A-33	US-10-369-493-24529	10-161-403-105	US-10-432-777-16	10-817-950-	US-10-109-853-13	24 US-11-006-076-109	US-10-161-408-21	US-10-161-403-109	US-11-006-076-108	US-10-161-403-108	US-10-757-093-7	US-10-364-649-27	US-10-757-093-9	US-10-322-656-48	6-4	-10-120-145-7	10-757-093	-10-421-175-3	-10-388-934-2	-10-335-053-	70.0	10-388-360-3	-10-388-360-3
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Sequence 14, Application US/10364649

Publication No. US20030229921A1

GENERAL INFORMATION:
APPLICANT: Richard A. Jefferson and Jorge E. Mayer
TITLE OF INVENTION: MICROBLAL B-GLUCURONIDASE GENES, GENE
TITLE OF INVENTION: PRODUCTS, AND USES THEREOF
FILE REFERENCE: 190106.405C1
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: US/10/364,649
PRIOR FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: US 99/270,957
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 1689
TYPE: DNA
ORGANISM: Thermotoga maritima
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(1689)
OTHER INFORMATION: n = A,T,C or G
US-10-364-649-14

Ouery Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1689; Conservative 0; Mismatches 0; Indels 0; Gaps
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GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 26682
TYPE: DNA
ORGANISM: Thermotoga maritima
US-10-369-493-26682
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US-10-369-493-26682
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Sequence 1, Application US/10757093;
Publication No. US20050153448A1;
GENERAL INFORMATION:
APPLICANT: CAMBIA
TITLE OF INVENTION: Fungal beta-glucuronidase ger
FILE REFERENCE: 415;
CURRENT APPLICATION NUMBER: US/10/757,093;
CURRENT FILING DATE: 2004-01-14;
NUMBER OF SEQ ID NOS: 37;
SOFTWARE: Patentin version 3.2;
SEQ ID NO 1
LENGTH: 1926;
TYPE: DNA
ORGANISM: Scopulariopsis sp. isoate RP38.3;
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CURRENT FILING DATE: 2002-08-22
PRIOR APPLICATION NUMBER: US 60/287,531
PRIOR FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: US 60/304,609
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/329,461
PRIOR FILING DATE: 2001-10-15
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/351,276
PRIOR APPLICATION NUMBER: US 60/351,276
PRIOR FILING DATE: 2002-01-23
NUMBER OF SEQ ID NOS: 22
CORPENSATE PRIOR SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.0 SEQ ID NO 5 LENGTH: 2169
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                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LeBowitz, Jonathan
APPLICANT: Beverley, Stephen
TITLE OF INVENTION: SUBCELLULAR TARGETING
FILE REFERENCE: SYM-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: A recombinant sequence incorporating a signal peptide sequence, OTHER INFORMATION: the mature human beta-glucuronidase sequence, a bridge of three OTHER INFORMATION: amino acids, and an IGF-II sequence
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LOCATION: (1)..(2166)
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                                                                                                                                                                                                                                                              Sequence 5, Application US/10272531A Publication No. US20040005309A1 GENERAL INFORMATION:
APPLICANT: LeBowitz, Jonathan H
APPLICANT: Beverley, Stephen
APPLICANT: Sly, William S.
TITLE OF INVENTION: TARGETED THERAPEUTIC PROTEINS
FILE REFERENCE: SYM-009
CURRENT APPLICATION NUMBER: US/10/272,531A
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: US 60/384,452
PRIOR FILING DATE: 2002-05-29
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PRIOR APPLICATION NUMBER: US 60/386,019
PRIOR FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: US 60/408,816
PRIOR FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 2169
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Best Local Similarity 52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: A recombinant DNA sequence incorporating a signal peptide sequence OTHER INFORMATION: e, the mature human beta-glucuronidase sequence, a bridge of three OTHER INFORMATION: e amino acids, and an IGF-II sequence FEATURE:

NAME/KEY: CDS
LOCATION: (1)..(2166)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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ATAAGAAGTATCAGAAGCCCATTATTCAGAGCGAGTATGGAGCAGAAACGATTGCAGGGT
                                                                                    ACGACTACGGGCACCTGGAGTTGATTCAGCTGCCAGCTGGCCACCCAGTTTGAGAACTGGT
                                                                                                                            TCTATCAGGGAAGGATAGAAGAAGGACTTCAAGCTCTGGAAAAAGACATAGAAGAGCTCT
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                                      ATGCAAGGCACAGAAAGCCCATCTTTGTCACAGAATTCGGTGCGGACGCGATAGCTGGCA
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US-10-272-483A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version
; SEQ ID NO 5
; LENGTH: 2169
; TYPE: DNA
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                                                                                                                                                                                                                     Matches 493;
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/272,483A
CURRENT FILING DATE: 2002-10-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/287,531 PRIOR FILING DATE: 2001-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Beverley, Stephen
TITLE OF INVENTION: TARGETED THERAPEUTIC PROTEINS
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                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (1)..(2166)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: A recombinant DNA sequence incorporating a signal peptide sequence OTHER INFORMATION: e, the mature human beta-glucuronidase sequence, a bridge of thre OTHER INFORMATION: e amino acids, and an IGF-II sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2002-06-05
APPLICATION NUMBER: US 60/408,816
FILING DATE: 2002-09-06
APPLICATION NUMBER: US 60/304,609
FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/384,452 FILING DATE: 2002-05-29 APPLICATION NUMBER: US 60/386,019
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    AATTCCCCGGTTCTGGGGGCAGGGCACCTTTATCCATTGATGATAAAAGACTTCAACCTTC
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                                                              AGAGCCAGTTCCTCATCAATGGGAAACCTTTCTATTTCCACGGTGTCAACAAGCATGAGG
                                                                                                 AGAAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGCTTTGGAAAGCACGAGG
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                                                                                                                                                                                                                 Score 174; DB 17;
Pred. No. 9.8e-45;
0; Mismatches 430
                                                                                                                                                                                                                     430;
                                                                                                                                                                                                                                                     Length 2169;
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APPLICANT: Couto, Linda B.
APPLICANT: Yang, Bin
TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIR
TITLE OF INVENTION: TREATMENT OF LYSOSOMAL DISORDERS
FILE REFERICE: 0800-0021
CURRENT APPLICATION NUMBER: US/10/421,175
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: US/09/715,858
PRIOR APPLICATION NUMBER: US/09/715,858
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
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US-10-421-175-1
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                                                                                                                                                                                                                                                                        Sequence 1, Application US/10421175 Publication No. US20030219414A1
                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                   APPLICANT: Podsakoff, Gregory APPLICANT: Watson, Gordon
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                                                                                                                                                                                  Watson, Gorange Pointo, Linda B.
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TYPE: DNA
ORGANISM: Homo Bapiens
FEATURE:
NAME/KEY: CDS
; LOCATION: (1)..(1956)
US-10-421-175-1
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                                                                                  ACGATCAGGCTCCTTTTGAAAAA-----AGACTACATCATCGGAACACACGTGTGGGCCT
                                                                                                                      TTCACCAGGATCCACCTCTGATGTTCACTGAAGAGTACCAGAAAAGTCTGCTAGAGCAGT
                                                                                                                                                TCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAGCTCGTTGAAAAG-
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 TTGCCGATTTCATGACTGAACAGTCACCGACGAGAGTGCTGGGGGAATAAAAAGGGGGATCT
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Sequence 343, Application US/10388360; Publication No. US20030225528A1; GENERAL INFORMATION:
APPLICANT: GENOMIC HEALTH; APPLICANT: Baker, Joffre B.
APPLICANT: Cronin, Maureen T.
APPLICANT: Kiefer, Michael C.
APPLICANT: Shak, Steve
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FITTE OF INVENTION: GENE EXPRESSION PROFILING IN
FILE REFERENCE: 39740-0001US
CURRENT APPLICATION NUMBER: US/10/388,360
CURRENT FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 60/412,049
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US 60/364,890
PRIOR FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 384
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 GAGACGTGGCGCTGAAGTACTTCGACATCGTCTGTGTGAACAGGTACTACGGCTGGTACA 1333
                                                                                                                                  AGTCCAACCATCCAGACGCGGAGGGTTTCTTCAAAGCCCCTTTATGAGACTGCCAATGAAA 1213
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                                  TGGACCCCTCCCGGCCTGTGACCTTTGTGAGCAACTCTAACTATGCAG----
                                                                 TGGATCGAACACGCCCCGTTGTCATGGTGAGCATGATGGACGCACCAGACGAGAGAACAA
                                                                                                   CGTCCCACCTAGAATCTGCTGGCTACTTGAAGATGGTGATCGCTCACACCAAATCCT
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Pred. No. 3.3e-44;
0; Mismatches 431;
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PRIOR APPLICATION NUMBER: 60/377,672
PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 2191
TYPE: DNA
ORGANISM: Homo sapiens
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US-10-429-802-16
; Sequence 16, Application US/10429802
; Publication No. US20030228285A1
; GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: BIPARTITE T-CELL FACT
FILE REFERENCE: UTSC:752US
CURRENT APPLICATION NUMBER: US/10/429,802
CURRENT FILING DATE: 2003-05-05
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      TGCAGATGTGACCGCTATGGGATTGTGGTCATCGATGAGTGTCCCGGCGTGGGCCTGG
                                                                               TTCGCTGGCTTGGTGCCAACGCTTTCCGTACCAGCCACTACCCCTATGCAGAGGAAGTGA
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                                        TGGATCTTGCCGACAGACTCGGAATCCTTGTGATAGACGAAGCCCCGGCACGTTGGTATCA
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ZOU, YIYU
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; Sequence 7, Application US/10430503
; Publication No. US20040005684A1
; GENERAL INFORMATION:
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                                                              US-10-430-503-7
                                                                                                                                     SOFTWARE: PatentIn Ver. SEQ ID NO 7
Query Match
Best Local Similarity
                                                                                                                                                     FILE REFERENCE: UTSC:797US
CURRENT APPLICATION NUMBER: US/10/430,
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/383,063
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                              APPLICANT: HUNG, MIEN-CHIE APPLICANT: LAN, KENG-LI APPLICANT: OU-YANG, FU APPLICANT: LIU, JAW-CHING APPLICANT: LAN, KENG-HSIN
                                                                          LENGTH: 2191
TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: TARGETING TITLE OF INVENTION: REAGENTS
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52.1%;
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   Score 172.4; DB 1
Pred. No. 3.3e-44;
                    DB 17;
                     Length
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1671

1611 1393 1491 1273 1383

1851 1627 1567 1731

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RESULT 11
US-10-335-053-51
; Sequence 51, Application US/10335053
; Publication No. US20040241653A1
; GENERAL INFORMATION:
; APPLICANT: Quark Biotech, Inc.
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Best Local S
Matches 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Methods for identifying marker genes for cancer FILE REFERENCE: 68733-A; 070/US1
CURRENT APPLICATION NUMBER: US/10/335,053
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: 60/345,317
PRIOR FILING DATE: 2001-12-31
NUMBER OF SEQ ID NOS: 319
SOFTWARE: PatentIn version 3.2
SEQ ID NO 51
LENGTH: 2191
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                                          ACGATCAGGCTCCTTTTGAAAAA-----AGACTACATCATCGGAACACACGTGTGGGCCT
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nilarity 52.1%;
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Pred. No. 3.3e-44;
0; Mismatches 431;
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CURRENT APPLICATION NUMBER: US/10/388,934
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 02005336.9
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 02015657.6
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 862
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 225
; LENGTH: 2472
; TYPE: DNA
; ORGANISM: Rattus norvegicus (No. US20040005547Alway rat)
US-10-388-934-225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.9%; Score 166.8; DB 17; Length Best Local Similarity 51.3%; Pred. No. 2.3e-42; Matches 477; Conservative 0; Mismatches 432; Indels
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APPLICANT: Suter-Dick, Lau
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TITLE OF INVENTION: BIOMARKERS AND EXPRESSION
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                             CCCGTTGTCATGGTGAGCATGGACGCACCAGACGAGAGAACAAGAGACGTGGCGCTG
                                                                          CCTGCCGGATATTACTTCAAGACGCTGATCGCCCACACCAAAGCCCCTGGACCCCACCCGT
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   CCTGTGACCTTTGTGAGCAATA--
                                                                                                   GACGCGGAGGGTTTCTTCAAAAGCCCTTTATGAGACTGCCAATGAAATGGATCGAACACGC
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Wolf, Detlef
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 -CCAGATATGACGCAGACATGGGGGCC
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RESULT 13
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; LENGTH: 1947
; TYPE: DNA
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Best Local Similarity 50.6%;
Matches 477; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Podsakoff, Gregory
APPLICANT: Watson, Gordon
APPLICANT: Watson, Gordon
APPLICANT: Couto, Linda B.
APPLICANT: Yang, Bin
TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
TITLE OF INVENTION: TREATMENT OF LYSOSOMAL DISORDERS
FILE REFERENCE: 0800-0021
CURRENT APPLICATION NUMBER: US/10/421,175
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: US/09/715,858
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1947)
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 TCAGATATCCGAGGGAAAGGCTTCGACTGGCCGCTGCTAAAGGATTTCAACCTGCTC
                                                                                                                     AAGAGGCTCTATCTGAACGGGAAACCTGTCTTTTTGAAGGGCTTTGGAAAGCACGAGGAA 858
                                                                                                                                                               GAGTCTGTGACTACTACACCCTTCCTATCGGGATTCGAACAGTGGCTGTCACAAAG
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                                     TTCCCCGTTCTGGGGCAGGGCACCTTTTATCCATTGATGATAAAAGACTTCAACCTTCTG
                                                                                AGCAAGTTCCTCATAAACGGGAAGCCCTTCTATTTCCAAGGGGTCAATAAGCACGAGGAT
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                                                                                                                                                                                                                                          Score 159.6; DB 17; Length 1947; Pred. No. 4.4e-40; 0; Mismatches 444; Indels 21;
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Sequence 3, Application US/10757093
; Publication No. US20050153448A1
; GENERAL INFORMATION:
    APPLICANT: CAMBIA
    TITLE OF INVENTION: Fungal beta-glucuronidase gen
; FILE REFERENCE: 415
; CURRENT APPLICATION NUMBER: US/10/757,093
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1905
; TYPE: DNA
; ORGANISM: Penicillium canescens isolate RPK
US-10-757-093-3
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APPLICANT: Jefferson, Richard A.
APPLICANT: Kilian, Andrzej
APPLICANT: Kilian, Andrzej
APPLICANT: Keese, Paul Konrad
TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, G
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 190106.405
CURRENT APPLICATION NUMBER: US/10/120,145
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/
PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-08
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 1887
TYPE: DNA
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Best Local Similarity
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Publication No. US20030157684A1
GENERAL INFORMATION:
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ORGANISM: Bacillus
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Pred. No. 3.5e-34;
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Search completed: September 1, 2005, 21:26:50 Job time : 1170 secs